

SEQUENCE LISTING

<110> Saba, Julie D.

<120> COMPOSITIONS AND METHODS FOR THE MODULATION
OF SPHINGOLIPID METABOLISM AND/OR SIGNALING

<130> 200116.405C1

<140> US

<141> 2003-07-16

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<213> S. cerevisiae

<220>

<221> CDS

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att cta acc atc aac gaa tta aaa ata gcc ata cat ggt tac ctc aga 144
Ile Leu Thr Ile Asn Glu Leu Lys Ile Ala Ile His Gly Tyr Leu Arg
35 40 45

aat acc cca tgg tac aac atg ttg aag gat tat ttg ttt gtg atc ttt 192
Asn Thr Pro Trp Tyr Asn Met Leu Lys Asp Tyr Leu Phe Val Ile Phe
50 55 60

tgt tac aag cta ata agt aat ttg ttt tat ctg ttg aaa gtt tat ggg 240
Cys Tyr Lys Leu Ile Ser Asn Phe Phe Tyr Leu Leu Lys Val Tyr Gly
65 70 75 80

ccg gtg agg tta gca gtg aga aca tac gag cat agt tcc aga aga ttg 288
Pro Val Arg Leu Ala Val Arg Thr Tyr Glu His Ser Ser Arg Arg Leu
85 90 95

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gaa gtc aca aag gtc aaa caa tcg atc gaa gac gaa cta att aga tcg Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser 115 120 125	384
gac tct cag tta atg aat ttc cca cag ttg cca tcc aat ggg ata cct Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro 130 135 140	432
cag gat gat gtt att gaa gag cta aat aaa ttg aac gac ttg ata cca Gln Asp Asp Val Ile Glu Glu Leu Asn Lys Leu Asn Asp Leu Ile Pro 145 150 155 160	480
cat acc caa tgg aag gaa gga aag gtc tct ggt gcc gtt tac cac ggt His Thr Gln Trp Lys Glu Gly Lys Val Ser Gly Ala Val Tyr His Gly 165 170 175	528
ggt gat gat ttg atc cac tta caa aca atc gca tac gaa aaa tat tgc Gly Asp Asp Leu Ile His Leu Gln Thr Ile Ala Tyr Glu Lys Tyr Cys 180 185 190	576
gtt gcc aat caa tta cat ccc gat gtc ttt cct gcc gta cgt aaa atg Val Ala Asn Gln Leu His Pro Asp Val Phe Pro Ala Val Arg Lys Met 195 200 205	624
gaa tcc gaa gtg gtt tct atg gtt tta aga atg ttt aat gcc cct tct Glu Ser Glu Val Val Ser Met Val Leu Arg Met Phe Asn Ala Pro Ser 210 215 220	672
gat aca ggt tgt ggt acc aca act tca ggt ggt aca gaa tcc ttg ctt Asp Thr Gly Cys Gly Thr Thr Ser Gly Gly Thr Glu Ser Leu Leu 225 230 235 240	720
tta gca tgt ctg agc gct aaa atg tat gcc ctt cat cat cgt gga atc Leu Ala Cys Leu Ser Ala Lys Met Tyr Ala Leu His His Arg Gly Ile 245 250 255	768
acc gaa cca gaa ata att gct ccc qta act qca cat qct qqq ttt gac Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp 260 265 270	816
aaa gct gct tat tac ttt ggc atg aag cta cgc cac gtg gag cta gat Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp 275 280 285	864
cca acg aca tat caa gtg gac ctg gga aaa gtg aaa aaa ttc atc aat Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn 290 295 300	912
aag aac aca att tta ctg gtc ggt tcc gct cca aac ttt cct cat ggt Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly	960

305	310	315	320	
att gcc gat gat att gaa gga ttg ggt aaa ata gca caa aaa tat aaa Ile Ala Asp Asp Ile Glu Gly Leu Gly Lys Ile Ala Gln Lys Tyr Lys 325		330	335	1008
ctt cct tta cac gtc gac agt tgt cta ggt tcc ttt att gtt tca ttt Leu Pro Leu His Val Asp Ser Cys Leu Gly Ser Phe Ile Val Ser Phe 340	345		350	1056
atg gaa aag gct ggt tac aaa aat ctg cca tta ctt gac ttt aga gtc Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Asp Phe Arg Val 355	360	365		1104
ccg gga gtc acc tca ata tca tgt gac act cat aaa tat gga ttt gca Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala 370	375	380		1152
cca aaa ggc tcg tca gtt ata atg tat aga aac agc gac tta cga atg Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met 385	390	395	400	1200
cat cag tat tac gta aat cct gct tgg act ggc ggg tta tat ggc tct His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser 405	410		415	1248
cct aca tta gca ggg tcc agg cct ggt gct att gtc gta ggt tgt tgg Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp 420	425		430	1296
gcc act atg gtc aac atg ggt gaa aat ggg tac att gag tcg tgc caa Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln 435	440	445		1344
gaa ata gtc ggt gca gca atg aag ttt aaa aaa tac atc cag gaa aac Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn 450	455	460		1392
att cca gac ctg aat ata atg ggc aac cct aga tat tca gtc att tca Ile Pro Asp Leu Asn Ile Met Gly Asn Pro Arg Tyr Ser Val Ile Ser 465	470	475	480	1440
ttt tct tca aag acc ttg aac ata cac gaa cta tct gac agg ttg tcc Phe Ser Ser Lys Thr Leu Asn Ile His Glu Leu Ser Asp Arg Leu Ser 485	490		495	1488
aag aaa ggc tgg cat ttc aat gcc cta caa aag ccg gtt gca cta cac Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His 500	505		510	1536
atg gcc ttc acg aga ttg agc gct cat gtt gtg gat gag atc tgc gac Met Ala Phe Thr Arg Leu Ser Ala His Val Val Asp Glu Ile Cys Asp 515	520	525		1584

att tta cgt act acc gtc caa gag ttg aag agc gaa tca aat tct aaa		1632	
Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys			
530	535	540	
cca tcc cca gac gga act agc gct cta tat ggt gtc gcc ggg agc gtt		1680	
Pro Ser Pro Asp Gly Thr Ser Ala Leu Tyr Gly Val Ala Gly Ser Val			
545	550	555	560
aaa act gct ggc gtt gca gac aaa ttg att gtg gga ttc cta gac gca		1728	
Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala			
565	570	575	
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580	585		

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Ile Leu Thr Ile Asn Glu Leu Lys Ile Ala Ile His Gly Tyr Leu Arg			
35	40	45	
Asn Thr Pro Trp Tyr Asn Met Leu Lys Asp Tyr Leu Phe Val Ile Phe			
50	55	60	
Cys Tyr Lys Leu Ile Ser Asn Phe Phe Tyr Leu Leu Lys Val Tyr Gly			
65	70	75	80
Pro Val Arg Leu Ala Val Arg Thr Tyr Glu His Ser Ser Arg Arg Leu			
85	90	95	
Phe Arg Trp Leu Leu Asp Ser Pro Phe Leu Arg Gly Thr Val Glu Lys			
100	105	110	
Glu Val Thr Lys Val Lys Gln Ser Ile Glu Asp Glu Leu Ile Arg Ser			
115	120	125	
Asp Ser Gln Leu Met Asn Phe Pro Gln Leu Pro Ser Asn Gly Ile Pro			
130	135	140	
Gln Asp Asp Val Ile Glu Glu Leu Asn Lys Leu Asn Asp Leu Ile Pro			
145	150	155	160
His Thr Gln Trp Lys Glu Gly Lys Val Ser Gly Ala Val Tyr His Gly			
165	170	175	
Gly Asp Asp Leu Ile His Leu Gln Thr Ile Ala Tyr Glu Lys Tyr Cys			
180	185	190	
Val Ala Asn Gln Leu His Pro Asp Val Phe Pro Ala Val Arg Lys Met			
195	200	205	
Glu Ser Glu Val Val Ser Met Val Leu Arg Met Phe Asn Ala Pro Ser			
210	215	220	
Asp Thr Gly Cys Gly Thr Thr Ser Gly Gly Thr Glu Ser Leu Leu			
225	230	235	240

Leu Ala Cys Leu Ser Ala Lys Met Tyr Ala Leu His His Arg Gly Ile
 245 250 255
 Thr Glu Pro Glu Ile Ile Ala Pro Val Thr Ala His Ala Gly Phe Asp
 260 265 270
 Lys Ala Ala Tyr Tyr Phe Gly Met Lys Leu Arg His Val Glu Leu Asp
 275 280 285
 Pro Thr Thr Tyr Gln Val Asp Leu Gly Lys Val Lys Lys Phe Ile Asn
 290 295 300
 Lys Asn Thr Ile Leu Leu Val Gly Ser Ala Pro Asn Phe Pro His Gly
 305 310 315 320
 Ile Ala Asp Asp Ile Glu Gly Leu Gly Lys Ile Ala Gln Lys Tyr Lys
 325 330 335
 Leu Pro Leu His Val Asp Ser Cys Leu Gly Ser Phe Ile Val Ser Phe
 340 345 350
 Met Glu Lys Ala Gly Tyr Lys Asn Leu Pro Leu Asp Phe Arg Val
 355 360 365
 Pro Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Phe Ala
 370 375 380
 Pro Lys Gly Ser Ser Val Ile Met Tyr Arg Asn Ser Asp Leu Arg Met
 385 390 395 400
 His Gln Tyr Tyr Val Asn Pro Ala Trp Thr Gly Gly Leu Tyr Gly Ser
 405 410 415
 Pro Thr Leu Ala Gly Ser Arg Pro Gly Ala Ile Val Val Gly Cys Trp
 420 425 430
 Ala Thr Met Val Asn Met Gly Glu Asn Gly Tyr Ile Glu Ser Cys Gln
 435 440 445
 Glu Ile Val Gly Ala Ala Met Lys Phe Lys Lys Tyr Ile Gln Glu Asn
 450 455 460
 Ile Pro Asp Leu Asn Ile Met Gly Asn Pro Arg Tyr Ser Val Ile Ser
 465 470 475 480
 Phe Ser Ser Lys Thr Leu Asn Ile His Glu Leu Ser Asp Arg Leu Ser
 485 490 495
 Lys Lys Gly Trp His Phe Asn Ala Leu Gln Lys Pro Val Ala Leu His
 500 505 510
 Met Ala Phe Thr Arg Leu Ser Ala His Val Val Asp Glu Ile Cys Asp
 515 520 525
 Ile Leu Arg Thr Thr Val Gln Glu Leu Lys Ser Glu Ser Asn Ser Lys
 530 535 540
 Pro Ser Pro Asp Gly Thr Ser Ala Leu Tyr Gly Val Ala Gly Ser Val
 545 550 555 560
 Lys Thr Ala Gly Val Ala Asp Lys Leu Ile Val Gly Phe Leu Asp Ala
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 <213> C. elegans

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ttt gag ctt cga aag ttc aat cca att gtt ctg gtt tct agt act att 96
Phe Glu Leu Arg Lys Phe Asn Pro Ile Val Leu Val Ser Ser Thr Ile
20 25 30

gtt gca aca tac gta ctc acc aat ctg aga cat atg cat tta gat gaa 144
Val Ala Thr Tyr Val Leu Thr Asn Leu Arg His Met His Leu Asp Glu
35 40 45

atg ggc atc cgg aaa cgt ttg agc act tgg ttt ttc acc act gta aag 192
Met Gly Ile Arg Lys Arg Leu Ser Thr Trp Phe Phe Thr Thr Val Lys
50 55 60

cgt gtg cct ttc atc agg aaa atg att gac aaa caa cta aac gaa gta 240
Arg Val Pro Phe Ile Arg Lys Met Ile Asp Lys Gln Leu Asn Glu Val
65 70 75 80

aag gac gag ctt gag aaa agt ctg aga att gtg gat cga agc acc gaa 288
Lys Asp Glu Leu Glu Lys Ser Leu Arg Ile Val Asp Arg Ser Thr Glu
85 90 95

tac ttc act aca atc cca agc cat tca gtt gga aga act gaa gta ctt 336
Tyr Phe Thr Thr Ile Pro Ser His Ser Val Gly Arg Thr Glu Val Leu
100 105 110

cgc ctt gct gcc atc tat gat gat ttg gaa gga cca gct ttt ttg gaa 384
Arg Leu Ala Ala Ile Tyr Asp Asp Leu Glu Gly Pro Ala Phe Leu Glu
115 120 125

gga aga gta tct gga gca gtc ttc aat aga gaa gac gac aag gac gaa 432
Gly Arg Val Ser Gly Ala Val Phe Asn Arg Glu Asp Asp Lys Asp Glu
130 135 140

cgg gag atg tat gag gag gtg ttc gga aaa ttt gcc tgg acc aac cca 480
Arg Glu Met Tyr Glu Glu Val Phe Gly Lys Phe Ala Trp Thr Asn Pro
145 150 155 160

ctt tgg cca aaa ttg ttc cct gga gtg aga atc atg gag gct gaa gtt 528
Leu Trp Pro Lys Leu Phe Pro Gly Val Arg Ile Met Glu Ala Glu Val
165 170 175

gtt cgc atg tgt tgt aat atg atg aat gga gat tcg gag aca tgt gga 576
Val Arg Met Cys Cys Asn Met Met Asn Gly Asp Ser Glu Thr Cys Gly
180 185 190

act atg tca act ggt gga tcc att tca att ctt ttg gcg tgc ctg gct 624
Thr Met Ser Thr Gly Gly Ser Ile Ser Ile Leu Leu Ala Cys Leu Ala
195 200 205

cat cgt aat cgt ctt ttg aaa aga gga gaa aag tac aca gag atg att		672	
His Arg Asn Arg Leu Leu Lys Arg Gly Glu Lys Tyr Thr Glu Met Ile			
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Val Pro Ser Ser Val His Ala Ala Phe Phe Lys Ala Ala Glu Cys Phe			
225	230	235	240
cgt atc aaa gtt cgc aag att cca gtt gat cct gtt act ttc aaa gta		768	
Arg Ile Lys Val Arg Lys Ile Pro Val Asp Pro Val Thr Phe Lys Val			
245	250	255	
gac ctt gtc aaa atg aaa gcc gca att aac aag aga aca tgt atg tta		816	
Asp Leu Val Lys Met Lys Ala Ala Ile Asn Lys Arg Thr Cys Met Leu			
260	265	270	
gtt gga tct gct cca aac ttt cca ttt gga act gtt gat gac att gaa		864	
Val Gly Ser Ala Pro Asn Phe Pro Phe Gly Thr Val Asp Asp Ile Glu			
275	280	285	
gct att gga cag cta gga ctt gaa tat gac atc cca gtt cat gtt gat		912	
Ala Ile Gly Gln Leu Gly Leu Glu Tyr Asp Ile Pro Val His Val Asp			
290	295	300	
gct tgt ctt ggt ggt ttc ctt cca ttc ctt gaa gaa gac gag att		960	
Ala Cys Leu Gly Gly Phe Leu Leu Pro Phe Leu Glu Glu Asp Glu Ile			
305	310	315	320
cgc tat gac ttc cgt gtt cct ggt gta tct tcg att tct gca gat agt		1008	
Arg Tyr Asp Phe Arg Val Pro Gly Val Ser Ser Ile Ser Ala Asp Ser			
325	330	335	
cac aaa tac gga ctc gct cca aag ggg tca tca gtt gtt ctt tat cgc		1056	
His Lys Tyr Gly Leu Ala Pro Lys Gly Ser Ser Val Val Leu Tyr Arg			
340	345	350	
aat aag gaa ctt ctt cat aat cag tac ttc tgt gat gct gat tgg caa		1104	
Asn Lys Glu Leu Leu His Asn Gln Tyr Phe Cys Asp Ala Asp Trp Gln			
355	360	365	
gga ggt atc tat gca tcg gct act atg gaa gga tca cgc gct ggg cac		1152	
Gly Gly Ile Tyr Ala Ser Ala Thr Met Glu Gly Ser Arg Ala Gly His			
370	375	380	
aac att gca ctt tgc tgg gcc gca atg ctt tat cac gct cag gaa gga		1200	
Asn Ile Ala Leu Cys Trp Ala Ala Met Leu Tyr His Ala Gln Glu Gly			
385	390	395	400
tac aag gcc aat gct aga aag att gtt gac act aca aga aag att aga		1248	
Tyr Lys Ala Asn Ala Arg Lys Ile Val Asp Thr Thr Arg Lys Ile Arg			
405	410	415	
aat gga ctt tca aac att aag gga atc aaa tta caa ggg cca agt gat		1296	
Asn Gly Leu Ser Asn Ile Lys Gly Ile Lys Leu Gln Gly Pro Ser Asp			

420	425	430	
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435	440	445	
ttc cat aac ttc atg aag gaa aaa cat tgg caa ctg aat gga ctt caa Phe His Asn Phe Met Lys Glu Lys His Trp Gln Leu Asn Gly Leu Gln			1392
450	455	460	
ttc cca gct gga gtt cat atc atg gtc act atg aat cat act cat cct Phe Pro Ala Gly Val His Ile Met Val Thr Met Asn His Thr His Pro			1440
465	470	475	480
gga ctc gct gaa gct ttc gtc gcc gat tgc aga gct gca gtt gag ttt Gly Leu Ala Glu Ala Phe Val Ala Asp Cys Arg Ala Ala Val Glu Phe			1488
485	490	495	
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500	505	510	
atc tac gga ctt gct caa agt att cca gac cga tcg ctt gtt cac gag Ile Tyr Gly Leu Ala Gln Ser Ile Pro Asp Arg Ser Leu Val His Glu			1584
515	520	525	
ttt gct cac agc tat atc gat gct gtt tat gct tta aca gag tga Phe Ala His Ser Tyr Ile Asp Ala Val Tyr Ala Leu Thr Glu *			1629
530	535	540	

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Val Ala Thr Tyr Val Leu Thr Asn Leu Arg His Met His Leu Asp Glu			
35	40	45	
Met Gly Ile Arg Lys Arg Leu Ser Thr Trp Phe Phe Thr Thr Val Lys			
50	55	60	
Arg Val Pro Phe Ile Arg Lys Met Ile Asp Lys Gln Leu Asn Glu Val			
65	70	75	80
Lys Asp Glu Leu Glu Lys Ser Leu Arg Ile Val Asp Arg Ser Thr Glu			
85	90	95	
Tyr Phe Thr Thr Ile Pro Ser His Ser Val Gly Arg Thr Glu Val Leu			
100	105	110	
Arg Leu Ala Ala Ile Tyr Asp Asp Leu Glu Gly Pro Ala Phe Leu Glu			
115	120	125	

Gly Arg Val Ser Gly Ala Val Phe Asn Arg Glu Asp Asp Lys Asp Glu
 130 135 140
 Arg Glu Met Tyr Glu Glu Val Phe Gly Lys Phe Ala Trp Thr Asn Pro
 145 150 155 160
 Leu Trp Pro Lys Leu Phe Pro Gly Val Arg Ile Met Glu Ala Glu Val
 165 170 175
 Val Arg Met Cys Cys Asn Met Met Asn Gly Asp Ser Glu Thr Cys Gly
 180 185 190
 Thr Met Ser Thr Gly Gly Ser Ile Ser Ile Leu Leu Ala Cys Leu Ala
 195 200 205
 His Arg Asn Arg Leu Leu Lys Arg Gly Glu Lys Tyr Thr Glu Met Ile
 210 215 220
 Val Pro Ser Ser Val His Ala Ala Phe Phe Lys Ala Ala Glu Cys Phe
 225 230 235 240
 Arg Ile Lys Val Arg Lys Ile Pro Val Asp Pro Val Thr Phe Lys Val
 245 250 255
 Asp Leu Val Lys Met Lys Ala Ala Ile Asn Lys Arg Thr Cys Met Leu
 260 265 270
 Val Gly Ser Ala Pro Asn Phe Pro Phe Gly Thr Val Asp Asp Ile Glu
 275 280 285
 Ala Ile Gly Gln Leu Gly Leu Glu Tyr Asp Ile Pro Val His Val Asp
 290 295 300
 Ala Cys Leu Gly Gly Phe Leu Leu Pro Phe Leu Glu Glu Asp Glu Ile
 305 310 315 320
 Arg Tyr Asp Phe Arg Val Pro Gly Val Ser Ser Ile Ser Ala Asp Ser
 325 330 335
 His Lys Tyr Gly Leu Ala Pro Lys Gly Ser Ser Val Val Leu Tyr Arg
 340 345 350
 Asn Lys Glu Leu Leu His Asn Gln Tyr Phe Cys Asp Ala Asp Trp Gln
 355 360 365
 Gly Ile Tyr Ala Ser Ala Thr Met Glu Gly Ser Arg Ala Gly His
 370 375 380
 Asn Ile Ala Leu Cys Trp Ala Ala Met Leu Tyr His Ala Gln Glu Gly
 385 390 395 400
 Tyr Lys Ala Asn Ala Arg Lys Ile Val Asp Thr Thr Arg Lys Ile Arg
 405 410 415
 Asn Gly Leu Ser Asn Ile Lys Gly Ile Lys Leu Gln Gly Pro Ser Asp
 420 425 430
 Val Cys Ile Val Ser Trp Thr Thr Asn Asp Gly Val Glu Leu Tyr Arg
 435 440 445
 Phe His Asn Phe Met Lys Glu Lys His Trp Gln Leu Asn Gly Leu Gln
 450 455 460
 Phe Pro Ala Gly Val His Ile Met Val Thr Met Asn His Thr His Pro
 465 470 475 480
 Gly Leu Ala Glu Ala Phe Val Ala Asp Cys Arg Ala Ala Val Glu Phe
 485 490 495
 Val Lys Ser His Lys Pro Ser Glu Ser Asp Lys Thr Ser Glu Ala Ala
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 Ile Tyr Gly Leu Ala Gln Ser Ile Pro Asp Arg Ser Leu Val His Glu
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Glu Ile Leu Glu Ser Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly		
20	25	30

tat tgc acc aaa tat gag ccc tgg cag ctc att gcg tgg agt gtc ctg 144
 Tyr Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Leu
 35 40 45

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tgt act ctg ctg ata gtc tgg gtg tat gag ctt atc ttc cag cca gag    192
Cys Thr Leu Leu Ile Val Trp Val Tyr Glu Leu Ile Phe Gln Pro Glu
      50          55          60

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agt tta tgg tct cgg ttt aaa aaa aaa tta ttt aag ctt atc agg aag 240
Ser Leu Trp Ser Arg Phe Lys Lys Lys Leu Phe Lys Leu Ile Arg Lys
   65           70           75           80

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atg cca ttt att gga cgt aag atc gaa caa cag gtg agc aaa gcc aag 288
 Met Pro Phe Ile Gly Arg Lys Ile Glu Gln Gln Val Ser Lys Ala Lys
 85 90 95

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aag gat ctt gtc aag aac atg cca ttc cta aag gtg gac aag gat tat 336
Lys Asp Leu Val Lys Asn Met Pro Phe Leu Lys Val Asp Lys Asp Tyr
          100           105           110

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gtg aaa act ctg cct gct cag ggt atg ggc aca gct gag gtt ctg gag 384
 Val Lys Thr Leu Pro Ala Gln Gly Met Gly Thr Ala Glu Val Leu Glu
 115 120 125

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aga ctc aag gag tac agc tcc atg gat ggt tcc tgg caa gaa ggg aaa 432
Arg Leu Lys Glu Tyr Ser Ser Met Asp Gly Ser Trp Gln Glu Gly Lys
    130          135          140

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Ala Ser Gly Ala Val Tyr Asn Gly Glu Pro Lys Leu Thr Glu Leu Leu
145           150           155           160

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 165 170 175

atc ttc cct gga ttg cg ^g aag tta gag gca gaa atc gtt agg atg act Ile Phe Pro Gly Leu Arg Lys Leu Glu Ala Glu Ile Val Arg Met Thr 180 185 190	576
tgt tcc ctc ttc aat ggg gga cca gat tcc tgt gga tgt gtg act tct Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser 195 200 205	624
ggg gga acg gaa agc atc ctg atg gcc tgc aaa gct tac cgg gac ttg Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Tyr Arg Asp Leu 210 215 220	672
gcg tta gag aag ggg atc aaa act cca gaa att gtg gct ccc gag agt Ala Leu Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Glu Ser 225 230 240	720
gcc cat gct gca ttc gac aaa gca gct cat tat ttt ggg atg aag att Ala His Ala Ala Phe Asp Lys Ala Ala His Tyr Phe Gly Met Lys Ile 245 250 255	768
gtc cga gtt gca ctg aaa aag aac atg gag gtg gat gtg cag gca atg Val Arg Val Ala Leu Lys Lys Asn Met Glu Val Asp Val Gln Ala Met 260 265 270	816
aag aga gcc atc tcc agg aac aca gct atg ctg gtc tgt tct acc cca Lys Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro 275 280 285	864
cag ttt cct cat ggt gtg atg gat cct gtc ccc gaa gtg gcc aag tta Gln Phe Pro His Gly Val Met Asp Pro Val Pro Glu Val Ala Lys Leu 290 295 300	912
act gtc aga tat aaa atc cca ctc cat gtg gat gct tgt ctg ggg ggc Thr Val Arg Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly 305 310 315 320	960
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ttt gat ttc cgg g ^t gaa ggt gtg acc agc att tca gca gat act cat Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His 340 345 350	1056
aag tat ggc tat gct cct aaa ggt tca tca gtg gtg atg tac tct aac Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Val Val Met Tyr Ser Asn 355 360 365	1104
gag aag tac agg acg tac cag ttc ttt gtt ggt gca gac tgg caa ggt Glu Lys Tyr Arg Thr Tyr Gln Phe Phe Val Gly Ala Asp Trp Gln Gly 370 375 380	1152
ggt gtc tac gca tct cca agc ata gct ggc tca cgg cct ggt ggc atc Gly Val Tyr Ala Ser Pro Ser Ile Ala Gly Ser Arg Pro Gly Gly Ile	1200

385	390	395	400	
att gca gcc tgt tgg gcg gcc ttg atg cac ttc ggt gag aac ggc tat Ile Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr 405		410		415
gtt gaa gct acc aaa cag atc atc aaa act gct cgc ttc ctg aag tca Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser 420		425		430
gaa ctg gaa aac atc aaa aac atc ttc att ttc ggt gat cct caa ttg Glu Leu Glu Asn Ile Lys Asn Ile Phe Ile Phe Gly Asp Pro Gln Leu 435		440		445
tca gtt att gct ctg gga tcc aac gat ttt gac att tac cga cta tct Ser Val Ile Ala Leu Gly Ser Asn Asp Phe Asp Ile Tyr Arg Leu Ser 450		455		460
aat atg atg tct gct aag ggg tgg aat ttt aac tac ctg cag ttc cca Asn Met Met Ser Ala Lys Gly Trp Asn Phe Asn Tyr Leu Gln Phe Pro 465		470		475
aga agc att cat ttc tgc att acg tta gta cat act cgg aag cga gtg Arg Ser Ile His Phe Cys Ile Thr Leu Val His Thr Arg Lys Arg Val 485		490		495
gcg atc cag ttc cta aag gat atc cgg gaa tca gtc aca caa atc atg Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met 500		505		510
aag aat cct aaa gct aag acc aca gga atg ggt gcc atc tat ggc atg Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Gly Met 515		520		525
gcc cag gca acc att gac agg aag ctg gtt gca gaa ata tcc tcc gtc Aia Gln Ala Thr Ile Asp Arg Lys Leu Val Ala Glu Ile Ser Ser Val 530		535		540
ttc ttg gac tgc ctt tat act acg gac ccc gtg act cag ggc aac cag Phe Leu Asp Cys Leu Tyr Thr Asp Pro Val Thr Gln Gly Asn Gln 545		550		555
atg aac ggt tct cca aag ccc cgc tga Met Asn Gly Ser Pro Lys Pro Arg *				560
565				

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<211> 568
<212> PRT
<213> Mus musculus

<400> 6
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1	5	10	15												
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			20				25					30			
Tyr	Cys	Thr	Lys	Tyr	Glu	Pro	Trp	Gln	Leu	Ile	Ala	Trp	Ser	Val	Leu
			35				40					45			
Cys	Thr	Leu	Leu	Ile	Val	Trp	Val	Tyr	Glu	Leu	Ile	Phe	Gln	Pro	Glu
			50				55					60			
Ser	Leu	Trp	Ser	Arg	Phe	Lys	Lys	Leu	Phe	Lys	Leu	Ile	Arg	Lys	
	65			70				75					80		
Met	Pro	Phe	Ile	Gly	Arg	Lys	Ile	Glu	Gln	Gln	Val	Ser	Lys	Ala	Lys
			85				90					95			
Lys	Asp	Leu	Val	Lys	Asn	Met	Pro	Phe	Leu	Lys	Val	Asp	Lys	Asp	Tyr
			100				105					110			
Val	Lys	Thr	Leu	Pro	Ala	Gln	Gly	Met	Gly	Thr	Ala	Glu	Val	Leu	Glu
			115				120					125			
Arg	Leu	Lys	Glu	Tyr	Ser	Ser	Met	Asp	Gly	Ser	Trp	Gln	Glu	Gly	Lys
			130				135					140			
Ala	Ser	Gly	Ala	Val	Tyr	Asn	Gly	Glu	Pro	Lys	Leu	Thr	Glu	Leu	Leu
	145				150				155					160	
Val	Gln	Ala	Tyr	Gly	Glu	Phe	Thr	Trp	Ser	Asn	Pro	Leu	His	Pro	Asp
			165				170					175			
Ile	Phe	Pro	Gly	Leu	Arg	Lys	Leu	Glu	Ala	Glu	Ile	Val	Arg	Met	Thr
			180				185					190			
Cys	Ser	Leu	Phe	Asn	Gly	Gly	Pro	Asp	Ser	Cys	Gly	Cys	Val	Thr	Ser
			195				200					205			
Gly	Gly	Thr	Glu	Ser	Ile	Leu	Met	Ala	Cys	Lys	Ala	Tyr	Arg	Asp	Leu
	210				215			220							
Ala	Leu	Glu	Lys	Gly	Ile	Lys	Thr	Pro	Glu	Ile	Val	Ala	Pro	Glu	Ser
	225				230			235					240		
Ala	His	Ala	Ala	Phe	Asp	Lys	Ala	Ala	His	Tyr	Phe	Gly	Met	Lys	Ile
			245				250					255			
Val	Arg	Val	Ala	Leu	Lys	Lys	Asn	Met	Glu	Val	Asp	Val	Gln	Ala	Met
			260				265					270			
Lys	Arg	Ala	Ile	Ser	Arg	Asn	Thr	Ala	Met	Leu	Val	Cys	Ser	Thr	Pro
			275				280					285			
Gln	Phe	Pro	His	Gly	Val	Met	Asp	Pro	Val	Pro	Glu	Val	Ala	Lys	Leu
			290				295					300			
Thr	Val	Arg	Tyr	Lys	Ile	Pro	Leu	His	Val	Asp	Ala	Cys	Leu	Gly	Gly
	305				310			315					320		
Phe	Leu	Ile	Val	Phe	Met	Glu	Lys	Ala	Gly	Tyr	Pro	Leu	Glu	Lys	Pro
			325				330					335			
Phe	Asp	Phe	Arg	Val	Lys	Gly	Val	Thr	Ser	Ile	Ser	Ala	Asp	Thr	His
			340				345					350			
Lys	Tyr	Gly	Tyr	Ala	Pro	Lys	Gly	Ser	Ser	Val	Val	Met	Tyr	Ser	Asn
			355				360					365			
Glu	Lys	Tyr	Arg	Thr	Tyr	Gln	Phe	Phe	Val	Gly	Ala	Asp	Trp	Gln	Gly
			370				375					380			
Gly	Val	Tyr	Ala	Ser	Pro	Ser	Ile	Ala	Gly	Ser	Arg	Pro	Gly	Gly	Ile
	385				390			395					400		
Ile	Ala	Ala	Cys	Trp	Ala	Ala	Leu	Met	His	Phe	Gly	Glu	Asn	Gly	Tyr
				405				410					415		
Val	Glu	Ala	Thr	Lys	Gln	Ile	Ile	Lys	Thr	Ala	Arg	Phe	Leu	Lys	Ser
			420				425					430			
Glu	Leu	Glu	Asn	Ile	Lys	Asn	Ile	Phe	Ile	Phe	Gly	Asp	Pro	Gln	Leu

435	440	445
Ser Val Ile Ala Leu Gly Ser Asn Asp Phe Asp Ile Tyr Arg Leu Ser		
450	455	460
Asn Met Met Ser Ala Lys Gly Trp Asn Phe Asn Tyr Leu Gln Phe Pro		
465	470	475
Arg Ser Ile His Phe Cys Ile Thr Leu Val His Thr Arg Lys Arg Val		480
485	490	495
Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met		
500	505	510
Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Gly Met		
515	520	525
Ala Gln Ala Thr Ile Asp Arg Lys Leu Val Ala Glu Ile Ser Ser Val		
530	535	540
Phe Leu Asp Cys Leu Tyr Thr Asp Pro Val Thr Gln Gly Asn Gln		
545	550	555
Met Asn Gly Ser Pro Lys Pro Arg		560
	565	

<210> 7
<211> 1707
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1707)

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Met Pro Ser Thr Asp Leu Leu Met Leu Lys Ala Phe Glu Pro Tyr Leu		
1	5	10
		15
gag att ttg gaa gta tac tcc aca aaa gcc aag aat tat gta aat gga	96	
Glu Ile Leu Glu Val Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly		
20	25	30
cat tgc acc aag tat gag ccc tgg cag cta att gca tgg agt gtc gtg	144	
His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val		
35	40	45
tgg acc ctg ctg ata gtc tgg gga tat gag ttt gtc ttc cag cca gag	192	
Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu		
50	55	60
agt tta tgg tca agg ttt aaa aag aaa tgt ttt aag ctc acc agg aag	240	
Ser Leu Trp Ser Arg Phe Lys Lys Cys Phe Lys Leu Thr Arg Lys		
65	70	75
		80
atg ccc att att ggt cgt aag att caa gac aag ttg aac aag acc aag	288	
Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys		
85	90	95
gat gat att agc aag aac atg tca ttc ctg aaa gtg gac aaa gag tat	336	

Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr			
100	105	110	
gtg aaa gct tta ccc tcc cag ggt ctg agc tca tct gct gtt ttg gag	384		
Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu			
115	120	125	
aaa ctt aag gag tac agc tct atg gac gcc ttc tgg caa gag ggg aga	432		
Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg			
130	135	140	
gcc tct gga aca gtg tac agt ggg gag gag aag ctc act gag ctc ctt	480		
Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu			
145	150	155	160
gtg aag gct tat gga gat ttt gca tgg agt aac ccc ctg cat cca gat	528		
Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp			
165	170	175	
atc ttc cca gga cta cgc aag ata gag gca gaa att gtg agg ata gct	576		
Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala			
180	185	190	
tgt tcc ctg ttc aat ggg gga cca gat tcg tgt gga tgt gtg act tct	624		
Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser			
195	200	205	
ggg gga aca gaa agc ata ctc atg gcc tgc aaa gca tgt cgg gat ctg	672		
Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Cys Arg Asp Leu			
210	215	220	
gcc ttt gag aag ggg atc aaa act cca gaa att gtg gct ccc caa agt	720		
Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser			
225	230	235	240
gcc cat gct gca ttt aac aaa gca gcc agt tac ttt ggg atg aag att	768		
Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile			
245	250	255	
gtg cgg gtc cca ttg acg aag atg atg gag gtg gat gtg agg gca atg	816		
Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met			
260	265	270	
aga aga gct atc tcc agg aac act gcc atg ctc gtc tgt tct acc cca	864		
Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro			
275	280	285	
cag ttt cct cat ggt gta ata gat cct gtc cct gaa gtg gcc aag ctg	912		
Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu			
290	295	300	
gct gtc aaa tac aaa ata ccc ctt cat gtc gac gct tgt ctg gga ggc	960		
Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly			
305	310	315	320

ttc ctc atc gtc ttt atg gag aaa gca gga tac cca ctg gag cac cca Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro 325 330 335	1008
ttt gat ttc cgg gtg aaa ggt gta acc agc att tca gct gac acc cat Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His 340 345 350	1056
aag tat ggc tat gcc cca aaa ggc tca tca ttg gtg ttg tat agt gac Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Leu Val Leu Tyr Ser Asp 355 360 365	1104
aag aag tac agg aac tat cag ttc ttc gtc gat aca gat tgg cag ggt Lys Lys Tyr Arg Asn Tyr Gln Phe Phe Val Asp Thr Asp Trp Gln Gly 370 375 380	1152
ggc atc tat gct tcc cca acc atc gca ggc tca cgg cct ggt ggc att Gly Ile Tyr Ala Ser Pro Thr Ile Ala Gly Ser Arg Pro Gly Gly Ile 385 390 395 400	1200
agc gca gcc tgt tgg gct gcc ttg atg cac ttc ggt gag aac ggc tat Ser Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr 405 410 415	1248
gtt gaa gct acc aaa cag atc atc aaa act gct cgc ttc ctc aag tca Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser 420 425 430	1296
gaa ctg gaa aat atc aaa ggc atc ttt gtt ttg ggg aat ccc caa ttg Glu Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu 435 440 445	1344
tca ctc att gct ctg gga tcc cgt gat ttt gac atc tac cga cta tca Ser Leu Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser 450 455 460	1392
aac ctg atg act gct aag ggg tgg aac ttg aac cag ttg cag ttc cca Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro 465 470 475 480	1440
ccc agt att cat ttc tgc atc aca tta cta cac gcc cgg aaa cga gta Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val 485 490 495	1488
gct ata caa ttc cta aag gac att cga gaa tct gtc actcaa atc atg Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met 500 505 510	1536
aag aat cct aaa gcg aag acc aca gga atg ggt gcc atc tat gcc atg Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Ala Met 515 520 525	1584
gcc cag aca act gtt gac agg aat atg gtt gca gaa ttg tcc tca gtc	1632

Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val			
530	535	540	
ttc ttg gac agc ttg tac agc acc gac act gtc acc cag ggc agc cag			1680
Phe Leu Asp Ser Leu Tyr Ser Thr Asp Thr Val Thr Gln Gly Ser Gln			
545	550	555	560
atg aat ggt tct cca aaa ccc cac tga			1707
Met Asn Gly Ser Pro Lys Pro His *			
565			

<210> 8
<211> 568
<212> PRT
<213> Homo sapiens

<400> 8			
Met Pro Ser Thr Asp Leu Leu Met Leu Lys Ala Phe Glu Pro Tyr Leu			
1	5	10	15
Glu Ile Leu Glu Val Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly			
20	25	30	
His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val			
35	40	45	
Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu			
50	55	60	
Ser Leu Trp Ser Arg Phe Lys Lys Cys Phe Lys Leu Thr Arg Lys			
65	70	75	80
Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys			
85	90	95	
Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr			
100	105	110	
Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu			
115	120	125	
Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg			
130	135	140	
Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu			
145	150	155	160
Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp			
165	170	175	
Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala			
180	185	190	
Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser			
195	200	205	
Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Cys Arg Asp Leu			
210	215	220	
Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser			
225	230	235	240
Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile			
245	250	255	
Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met			
260	265	270	
Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro			
275	280	285	

Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu
 290 295 300
 Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly
 305 310 315 320
 Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro
 325 330 335
 Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His
 340 345 350
 Lys Tyr Gly Tyr Ala Pro Lys Gly Ser Ser Leu Val Leu Tyr Ser Asp
 355 360 365
 Lys Lys Tyr Arg Asn Tyr Gln Phe Phe Val Asp Thr Asp Trp Gln Gly
 370 375 380
 Gly Ile Tyr Ala Ser Pro Thr Ile Ala Gly Ser Arg Pro Gly Gly Ile
 385 390 395 400
 Ser Ala Ala Cys Trp Ala Ala Leu Met His Phe Gly Glu Asn Gly Tyr
 405 410 415
 Val Glu Ala Thr Lys Gln Ile Ile Lys Thr Ala Arg Phe Leu Lys Ser
 420 425 430
 Glu Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu
 435 440 445
 Ser Leu Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser
 450 455 460
 Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro
 465 470 475 480
 Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val
 485 490 495
 Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met
 500 505 510
 Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Ala Met
 515 520 525
 Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val
 530 535 540
 Phe Leu Asp Ser Leu Tyr Ser Thr Asp Thr Val Thr Gln Gly Ser Gln
 545 550 555 560
 Met Asn Gly Ser Pro Lys Pro His
 565

<210> 9
 <211> 1467
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1467)

<400> 9
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 Met Pro Ser Thr Asp Leu Leu Met Leu Lys Ala Phe Glu Pro Tyr Leu
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gag att ttg gaa gta tac tcc aca aaa gcc aag aat tat gta aat gga 96
 Glu Ile Leu Glu Val Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly

20	25	30	
cat tgc acc aag tat gag ccc tgg cag cta att gca tgg agt gtc gtg His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val			144
35	40	45	
tgg acc ctg ctg ata gtc tgg gga tat gag ttt gtc ttc cag cca gag Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu			192
50	55	60	
agt tta tgg tca agg ttt aaa aag aaa tgt ttt aag ctc acc agg aag Ser Leu Trp Ser Arg Phe Lys Lys Cys Phe Lys Leu Thr Arg Lys			240
65	70	75	80
atg ccc att att ggt cgt aag att caa gac aag ttg aac aag acc aag Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys			288
85	90	95	
gat gat att agc aag aac atg tca ttc ctg aaa gtg gac aaa gag tat Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr			336
100	105	110	
gtg aaa gct tta ccc tcc cag ggt ctg agc tca tct gct gtt ttg gag Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ala Val Leu Glu			384
115	120	125	
aaa ctt aag gag tac agc tct atg gac gcc ttc tgg caa gag ggg aga Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg			432
130	135	140	
gcc tct gga aca gtg tac agt ggg gag gag aag ctc act gag ctc ctt Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu			480
145	150	155	160
gtg aag gct tat gga gat ttt gca tgg agt aac ccc ctg cat cca gat Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp			528
165	170	175	
atc ttc cca gga cta cgc aag ata gag gca gaa att gtg agg ata gct Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala			576
180	185	190	
tgt tcc ctg ttc aat ggg gga cca gat tcg tgt gga tgt gtg act tct Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser			624
195	200	205	
ggg gga aca gaa agc ata ctc atg gcc tgc aaa gca tgt cgg gat ctg Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Cys Arg Asp Leu			672
210	215	220	
gcc ttt gag aag ggg atc aaa act cca gaa att gtg gct ccc caa agt Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser			720
225	230	235	240

gcc cat gct gca ttt aac aaa gca gcc agt tac ttt ggg atg aag att Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile 245 250 255	768
gtg cgg gtc cca ttg acg aag atg atg gag gtg gat gtg agg gca atg Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met 260 265 270	816
aga aga gct atc tcc agg aac act gcc atg ctc gtc tgt tct acc cca Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro 275 280 285	864
cag ttt cct cat ggt gta ata gat cct gtc cct gaa gtg gcc aag ctg Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu 290 295 300	912
gct gtc aaa tac aaa ata ccc ctt cat gtc gac gct tgt ctg gga ggc Ala Val Lys Tyr Lys Ile Pro Leu His Val Asp Ala Cys Leu Gly Gly 305 310 315 320	960
ttc ctc atc gtc ttt atg gag aaa gca gga tac cca ctg gag cac cca Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro 325 330 335	1008
ttt gat ttc cgg gtg aaa ggt gta acc agc att tca gct gac acc cat Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His 340 345 350	1056
aag ctg gaa aat atc aaa ggc atc ttt gtt ttt ggg aat ccc caa ttg Lys Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu 355 360 365	1104
tca ctc att gct ctg gga tcc cgt gat ttt gac atc tac cga cta tca Ser Leu Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser 370 375 380	1152
aac ctg atg act gct aag ggg tgg aac ttg aac cag ttg cag ttc cca Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro 385 390 395 400	1200
ccc agt att cat ttc tgc atc aca tta cta cac gcc cgg aaa cqa gta Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val 405 410 415	1248
gct ata caa ttc cta aag gac att cga gaa tct gtc act caa atc atg Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met 420 425 430	1296
aag aat cct aaa gcg aag acc aca gga atg ggt gcc atc tat gcc atg Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Ala Met 435 440 445	1344
gcc cag aca act gtt gac agg aat atg gtt gca gaa ttg tcc tca gtc Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val	1392

450

455

460

ttc ttg gac agc ttg tac agc acc gac act gtc acc cag ggc agc cag 1440
 Phe Leu Asp Ser Leu Tyr Ser Thr Asp Thr Val Thr Gln Gly Ser Gln
 465 470 475 480

atg aat ggt tct cca aaa ccc cac tga 1467
 Met Asn Gly Ser Pro Lys Pro His *
 485

<210> 10
<211> 488
<212> PRT
<213> Homo sapiens

<400> 10
 Met Pro Ser Thr Asp Leu Leu Met Leu Lys Ala Phe Glu Pro Tyr Leu
 1 5 10 15
 Glu Ile Leu Glu Val Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly
 20 25 30
 His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val
 35 .. 40 45
 Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu
 50 55 60
 Ser Leu Trp Ser Arg Phe Lys Lys Cys Phe Lys Leu Thr Arg Lys
 65 70 75 80
 Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys
 85 90 95
 Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr
 100 105 110
 Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu
 115 120 125
 Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg
 130 135 140
 Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu
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 Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp
 165 170 175
 Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala
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 Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser
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 Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Cys Arg Asp Leu
 210 215 220
 Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser
 225 230 235 240
 Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile
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 Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met
 260 265 270
 Arg Arg Ala Ile Ser Arg Asn Thr Ala Met Leu Val Cys Ser Thr Pro
 275 280 285
 Gln Phe Pro His Gly Val Ile Asp Pro Val Pro Glu Val Ala Lys Leu

290	295	300
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305	310	315
Phe Leu Ile Val Phe Met Glu Lys Ala Gly Tyr Pro Leu Glu His Pro		
325	330	335
Phe Asp Phe Arg Val Lys Gly Val Thr Ser Ile Ser Ala Asp Thr His		
340	345	350
Lys Leu Glu Asn Ile Lys Gly Ile Phe Val Phe Gly Asn Pro Gln Leu		
355	360	365
Ser Leu Ile Ala Leu Gly Ser Arg Asp Phe Asp Ile Tyr Arg Leu Ser		
370	375	380
Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro		
385	390	395
Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val		
405	410	415
Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met		
420	425	430
Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Ala Met		
435	440	445
Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val		
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 <212> PRT
 <213> C. elegans

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35	40	45
Val His Leu Tyr Arg Lys Ser Glu Asp Pro Ile Leu Lys Arg Met Gly		
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Ala Tyr Val Phe Ser Leu Leu Arg Lys Leu Pro Ala Val Arg Asp Lys		
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Ile Glu Lys Glu Leu Ala Ala Glu Lys Pro Lys Leu Ile Glu Ser Ile		
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His Lys Asp Asp Lys Asp Lys Gln Phe Ile Ser Thr Leu Pro Ile Ala		
100	105	110
Pro Leu Ser Gln Asp Ser Ile Met Glu Leu Ala Lys Lys Tyr Glu Asp		
115	120	125
Tyr Asn Thr Phe Asn Ile Asp Gly Gly Arg Val Ser Gly Ala Val Tyr		
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Thr Asp Arg His Ala Glu His Ile Asn Leu Leu Gly Lys Ile Tyr Glu		
145	150	155
Lys Tyr Ala Phe Ser Asn Pro Leu His Pro Asp Val Phe Pro Gly Ala		

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Arg Lys Met Glu Ala Glu Leu Ile Arg Met Val Leu Asn Leu Tyr Asn			
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Gly Pro Glu Asp Ser Ser Gly Ser Val Thr Ser Gly Gly Thr Glu Ser			
195	200	205	
Ile Ile Met Ala Cys Phe Ser Tyr Arg Asn Arg Ala His Ser Leu Gly			
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Thr Ile Asp Pro Ile Pro Glu Ile Ala Lys Leu Gly Lys Lys Tyr Gly			
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305	310	315	320
Met Asn Asp Ala Gly Tyr Leu Ile Pro Val Phe Asp Phe Arg Asn Pro			
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Gly Val Thr Ser Ile Ser Cys Asp Thr His Lys Tyr Gly Cys Thr Pro			
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Lys Gly Ser Ser Ile Val Met Tyr Arg Ser Lys Glu Leu His His Phe			
355	360	365	
Gln Tyr Phe Ser Val Ala Asp Trp Cys Gly Gly Ile Tyr Ala Thr Pro			
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Thr Ile Ala Gly Ser Arg Ala Gly Ala Asn Thr Ala Val Ala Trp Ala			
385	390	395	400
Thr Leu Leu Ser Phe Gly Arg Asp Glu Tyr Val Arg Arg Cys Ala Gln			
405	410	415	
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420	425	430	
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435	440	445	
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450	455	460	
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465	470	475	480
Leu Thr Ile Asn Gln Ala Asn Glu Glu Val Val Asn Ala Phe Ala Val			
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<213> C. elegans

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<211> 545

<212> PRT

<213> Drosophila melanogaster

<400> 16

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									20		25			30	
Thr	Ala	Thr	Thr	Val	Leu	Gly	Gly	Val	Trp	Leu	Trp	Thr	Val	Ile	Cys
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Gln	Asp	Glu	Asn	Leu	Tyr	Ile	Arg	Gly	Lys	Arg	Gln	Phe	Phe	Lys	Phe
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Ala	Lys	Lys	Ile	Pro	Ala	Val	Arg	Arg	Gln	Val	Glu	Thr	Glu	Leu	Ala
									65		70			80	
Lys	Ala	Lys	Asn	Asp	Phe	Glu	Thr	Glu	Ile	Lys	Lys	Ser	Asn	Ala	His
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Leu	Thr	Tyr	Ser	Glu	Thr	Leu	Pro	Glu	Lys	Gly	Leu	Ser	Lys	Glu	Glu
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Val	Glu	Leu	Val	Thr	Glu	Val	Tyr	Gly	Ala	Ser	Tyr	Thr	Asn	Pro	
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Val	Arg	Met	Ala	Cys	Asn	Leu	Phe	His	Gly	Asn	Ser	Ala	Ser	Cys	Gly
									180		185			190	
Thr	Met	Thr	Thr	Gly	Gly	Thr	Glu	Ser	Ile	Val	Met	Ala	Met	Lys	Ala
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									210		215			220	
Val	Val	Pro	Lys	Thr	Val	His	Ala	Ala	Phe	Asp	Lys	Gly	Gly	Gln	Tyr
									225		230			240	
Phe	Asn	Ile	His	Val	Arg	Ser	Val	Asp	Val	Asp	Pro	Glu	Thr	Tyr	Glu
									245		250			255	
Val	Asp	Ile	Lys	Lys	Phe	Lys	Arg	Ala	Ile	Asn	Arg	Asn	Thr	Ile	Leu
									260		265			270	
Leu	Val	Gly	Ser	Ala	Pro	Asn	Phe	Pro	Tyr	Gly	Thr	Ile	Asp	Asp	Ile
									275		280			285	
Glu	Ala	Ile	Ala	Ala	Leu	Gly	Val	Lys	Tyr	Asp	Ile	Pro	Val	His	Val
									290		295			300	
Asp	Ala	Cys	Leu	Gly	Ser	Phe	Val	Val	Ala	Leu	Val	Arg	Asn	Ala	Gly
									305		310			315	
Tyr	Lys	Leu	Arg	Pro	Phe	Asp	Phe	Glu	Val	Lys	Gly	Val	Thr	Ser	Ile
									325		330			335	

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 Ile Leu Tyr Ser Asp Lys Lys Tyr Lys Asp His Gln Phe Thr Val Thr
 355 360 365
 Thr Asp Trp Pro Gly Gly Val Tyr Gly Ser Pro Thr Val Asn Gly Ser
 370 375 380
 Arg Ala Gly Gly Ile Ile Ala Ala Cys Trp Ala Thr Met Met Ser Phe
 385 390 395 400
 Gly Tyr Asp Gly Tyr Leu Glu Ala Thr Lys Arg Ile Val Asp Thr Ala
 405 410 415
 Arg Tyr Ile Glu Arg Gly Val Arg Asp Ile Asp Gly Ile Phe Ile Phe
 420 425 430
 Gly Lys Pro Ala Thr Ser Val Ile Ala Leu Gly Ser Asn Val Phe Asp
 435 440 445
 Ile Phe Arg Leu Ser Asp Ser Leu Cys Lys Leu Gly Trp Asn Leu Asn
 450 455 460
 Ala Leu Gln Phe Pro Ser Gly Ile His Leu Cys Val Thr Asp Met His
 465 470 475 480
 Thr Gln Pro Gly Val Ala Asp Lys Phe Ile Ala Asp Val Arg Ser Cys
 485 490 495
 Thr Ala Glu Ile Met Lys Asp Pro Gly Gln Pro Val Val Gly Lys Met
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 Lys
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 Glu Ile Leu Glu Val Tyr Ser Thr Lys Ala Lys Asn Tyr Val Asn Gly
 20 25 30

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 His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val
 35 40 45

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 Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu

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65	70	75	80
atg ccc att att ggt cgt aag att caa gac aag ttg aac aag acc aag			288
Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys			
85	90	95	
gat gat att agc aag aac atg tca ttc ctg aaa gtg gac aaa gag tat			336
Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr			
100	105	110	
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Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ala Val Leu Glu			
115	120	125	
aaa ctt aag gag tac agc tct atg gac gcc ttc tgg caa gag ggg aga			432
Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg			
130	135	140	
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Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu			
145	150	155	160
gtg aag gct tat gga gat ttt gca tgg agt aac ccc ctg cat cca gat			528
Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp			
165	170	175	
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Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala			
180	185	190	
tgt tcc ctg ttc aat ggg gga cca gat tcg tgt gga tgt gtg act tct			624
Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser			
195	200	205	
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Gly Gly Thr Glu Ser Ile Leu Met Ala Cys Lys Ala Tyr Arg Asp Leu			
210	215	220	
gcc ttt gag aag ggg atc aaa act cca gaa att gtg gct ccc caa agt			720
Ala Phe Glu Lys Gly Ile Lys Thr Pro Glu Ile Val Ala Pro Gln Ser			
225	230	235	240
gcc cat gct gca ttt aac aaa gca gcc agt tac ttt ggg atg aag att			768
Ala His Ala Ala Phe Asn Lys Ala Ala Ser Tyr Phe Gly Met Lys Ile			
245	250	255	
gtg cgg gtc cca ttg acg aag atg atg gag gtg gat gtg agg gca atg			816
Val Arg Val Pro Leu Thr Lys Met Met Glu Val Asp Val Arg Ala Met			
260	265	270	

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aac ctg atg act gct aag ggg tgg aac ttg aac cag ttg cag ttc cca Asn Leu Met Thr Ala Lys Gly Trp Asn Leu Asn Gln Leu Gln Phe Pro 465 470 475 480	1440
ccc agt att cat ttc tgc atc aca tta cta cac gcc cgaa aaa cga gta Pro Ser Ile His Phe Cys Ile Thr Leu Leu His Ala Arg Lys Arg Val	1488

485	490	495	
gct ata caa ttc cta aag gac att cga gaa tct gtc act caa atc atg Ala Ile Gln Phe Leu Lys Asp Ile Arg Glu Ser Val Thr Gln Ile Met			1536
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aag aat cct aaa gcg aag acc aca gga atg ggt gcc atc tat ggc atg Lys Asn Pro Lys Ala Lys Thr Thr Gly Met Gly Ala Ile Tyr Gly Met			1584
515	520	525	
gcc cag aca act gtt gac agg aat atg gtt gca gaa ttg tcc tca gtc Ala Gln Thr Thr Val Asp Arg Asn Met Val Ala Glu Leu Ser Ser Val			1632
530	535	540	
ttc ttg gac agc ttg tac agc acc gac act gtc acc cag ggc agc cag Phe Leu Asp Ser Leu Tyr Ser Thr Asp Thr Val Thr Gln Gly Ser Gln			1680
545	550	555	560
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565			

<210> 18
<211> 568
<212> PRT
<213> Homo sapiens

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His Cys Thr Lys Tyr Glu Pro Trp Gln Leu Ile Ala Trp Ser Val Val			
35	40	45	
Trp Thr Leu Leu Ile Val Trp Gly Tyr Glu Phe Val Phe Gln Pro Glu			
50	55	60	
Ser Leu Trp Ser Arg Phe Lys Lys Cys Phe Lys Leu Thr Arg Lys			
65	70	75	80
Met Pro Ile Ile Gly Arg Lys Ile Gln Asp Lys Leu Asn Lys Thr Lys			
85	90	95	
Asp Asp Ile Ser Lys Asn Met Ser Phe Leu Lys Val Asp Lys Glu Tyr			
100	105	110	
Val Lys Ala Leu Pro Ser Gln Gly Leu Ser Ser Ser Ala Val Leu Glu			
115	120	125	
Lys Leu Lys Glu Tyr Ser Ser Met Asp Ala Phe Trp Gln Glu Gly Arg			
130	135	140	
Ala Ser Gly Thr Val Tyr Ser Gly Glu Glu Lys Leu Thr Glu Leu Leu			
145	150	155	160
Val Lys Ala Tyr Gly Asp Phe Ala Trp Ser Asn Pro Leu His Pro Asp			
165	170	175	
Ile Phe Pro Gly Leu Arg Lys Ile Glu Ala Glu Ile Val Arg Ile Ala			
180	185	190	
Cys Ser Leu Phe Asn Gly Gly Pro Asp Ser Cys Gly Cys Val Thr Ser			

195	200	205													
Gly	Gly	Thr	Glu	Ser	Ile	Leu	Met	Ala	Cys	Lys	Ala	Tyr	Arg	Asp	Leu
210			215								220				
Ala	Phe	Glu	Lys	Gly	Ile	Lys	Thr	Pro	Glu	Ile	Val	Ala	Pro	Gln	Ser
225			230							235					240
Ala	His	Ala	Ala	Phe	Asn	Lys	Ala	Ala	Ser	Tyr	Phe	Gly	Met	Lys	Ile
										245		250			255
Val	Arg	Val	Pro	Leu	Thr	Lys	Met	Met	Glu	Val	Asp	Val	Arg	Ala	Met
										260		265			270
Arg	Arg	Ala	Ile	Ser	Arg	Asn	Thr	Ala	Met	Leu	Val	Cys	Ser	Thr	Pro
										275		280			285
Gln	Phe	Pro	His	Gly	Val	Ile	Asp	Pro	Val	Pro	Glu	Val	Ala	Lys	Leu
										290		295			300
Ala	Val	Lys	Tyr	Lys	Ile	Pro	Leu	His	Val	Asp	Ala	Cys	Leu	Gly	Gly
										305		310			320
Phe	Leu	Ile	Val	Phe	Met	Glu	Lys	Ala	Gly	Tyr	Pro	Leu	Glu	His	Pro
										325		330			335
Phe	Asp	Phe	Arg	Val	Lys	Gly	Val	Thr	Ser	Ile	Ser	Ala	Asp	Thr	His
										340		345			350
Lys	Tyr	Gly	Tyr	Ala	Pro	Lys	Gly	Ser	Ser	Leu	Val	Leu	Tyr	Ser	Asp
										355		360			365
Lys	Lys	Tyr	Arg	Asn	Tyr	Gln	Phe	Phe	Val	Asp	Thr	Asp	Trp	Gln	Gly
										370		375			380
Gly	Ile	Tyr	Ala	Ser	Pro	Thr	Ile	Ala	Gly	Ser	Arg	Pro	Gly	Gly	Ile
										385		390			400
Ser	Ala	Ala	Cys	Trp	Ala	Ala	Leu	Met	His	Phe	Gly	Glu	Asn	Gly	Tyr
										405		410			415
Val	Glu	Ala	Thr	Lys	Gln	Ile	Ile	Lys	Thr	Ala	Arg	Phe	Leu	Lys	Ser
										420		425			430
Glu	Leu	Glu	Asn	Ile	Lys	Gly	Ile	Phe	Val	Phe	Gly	Asn	Pro	Gln	Leu
										435		440			445
Ser	Val	Ile	Ala	Leu	Gly	Ser	Arg	Asp	Phe	Asp	Ile	Tyr	Arg	Leu	Ser
										450		455			460
Asn	Leu	Met	Thr	Ala	Lys	Gly	Trp	Asn	Leu	Asn	Gln	Leu	Gln	Phe	Pro
										465		470			480
Pro	Ser	Ile	His	Phe	Cys	Ile	Thr	Leu	Leu	His	Ala	Arg	Lys	Arg	Val
										485		490			495
Ala	Ile	Gln	Phe	Leu	Lys	Asp	Ile	Arg	Glu	Ser	Val	Thr	Gln	Ile	Met
										500		505			510
Lys	Asn	Pro	Lys	Ala	Lys	Thr	Thr	Gly	Met	Gly	Ala	Ile	Tyr	Gly	Met
										515		520			525
Ala	Gln	Thr	Thr	Val	Asp	Arg	Asn	Met	Val	Ala	Glu	Leu	Ser	Ser	Val
										530		535			540
Phe	Leu	Asp	Ser	Leu	Tyr	Ser	Thr	Asp	Thr	Val	Thr	Gln	Gly	Ser	Gln
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Met	Asn	Gly	Ser	Pro	Lys	Pro	His								
										565					

<210> 19
<211> 490

<212> PRT
<213> Drosophila melanogaster

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 35 40 45
 Gly Ser Gly Lys Gly Arg Glu Leu Phe Gln Lys Gln Val Ala Pro Leu
 50 55 60
 Leu Thr Glu Ala Glu Val Gln Tyr Asp Leu Gln Ile Thr Thr His Pro
 65 70 75 80
 Gln Tyr Ala Lys Glu Phe Val Arg Thr Arg Arg Asp Leu Leu Thr Arg
 85 90 95
 Tyr Ser Gly Ile Val Val Ala Ser Gly Asp Gly Leu Phe Tyr Glu Val
 100 105 110
 Leu Asn Gly Leu Met Glu Arg Met Asp Trp Arg Arg Ala Cys Arg Glu
 115 120 125
 Leu Pro Leu Gly Ile Ile Pro Cys Gly Ser Gly Asn Gly Leu Ala Lys
 130 135 140
 Ser Val Ala His His Cys Asn Glu Pro Tyr Glu Pro Lys Pro Ile Leu
 145 150 155 160
 His Ala Thr Leu Thr Cys Met Ala Gly Lys Ser Thr Pro Met Asp Val
 165 170 175
 Val Arg Val Glu Leu Ala Thr Arg Asp Lys His Phe Val Met Tyr Ser
 180 185 190
 Phe Leu Ser Val Gly Trp Gly Leu Ile Ala Asp Ile Asp Ile Glu Ser
 195 200 205
 Glu Arg Leu Arg Ser Ile Gly Ala Gln Arg Phe Thr Leu Trp Ala Ile
 210 215 220
 Lys Arg Leu Ile Gly Leu Arg Ser Tyr Lys Gly Arg Val Ser Tyr Leu
 225 230 235 240
 Leu Gly Lys Gly Lys Glu Pro Pro Val Glu Ala Ala Arg Glu Leu
 245 250 255
 Pro Ala Glu Ser Thr Ala Ala Gly Ile Arg Ser Ser Leu Pro Leu Asn
 260 265 270
 Ala Gly Glu Phe His Asp Leu Pro Glu Glu Glu Gly Glu Ala Val
 275 280 285
 Leu Asp Gly Glu Gln Phe Ala Asp Ala Ile Ser Leu Asp Arg Ser Val
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 Tyr Arg Gln His Ala Asp Ser Trp His Ser Ala Met Ser Arg Arg Thr
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 Ala Tyr Thr Thr His Leu Ser Ser Asp Val Phe Phe Ala Pro Glu Ser
 385 390 395 400
 Arg Leu Asp Asp Gly Leu Ile Tyr Leu Val Ile Ile Arg Arg Gly Val
 405 410 415
 Ser Arg His Gln Leu Leu Asn Phe Met Leu Asn Leu Asn Ala Gly Thr

420	425	430
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435	440	445
Ala Phe Arg Ile Glu Pro Ser Ser Ser Asp Gly Ile Leu Val Val Asp		
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465	470	475
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485	490	

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<212> PRT
<213> Drosophila melanogaster

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Phe Val Ala Pro Thr Val Asp Glu Arg Arg Arg Val Leu Val Leu		
35	40	45
Leu Asn Pro Lys Ser Gly Ser Gly Asp Ala Arg Glu Val Phe Asn Met		
50	55	60
His Val Thr Pro Val Leu Asn Glu Ala Glu Val Pro Tyr Asp Leu Tyr		
65	70	75
Val Thr Lys His Ser Asn Phe Ala Ile Glu Phe Leu Ser Thr Arg Cys		
85	90	95
Leu Asp Ala Trp Cys Cys Val Val Ala Val Gly Gly Asp Gly Leu Phe		
100	105	110
His Glu Ile Val Asn Gly Leu Leu Gln Arg Gln Asp Trp Ala His Val		
115	120	125
Leu Pro His Leu Ala Leu Gly Ile Ile Pro Cys Gly Ser Gly Asn Gly		
130	135	140
Leu Ala Arg Ser Ile Ala His Cys Tyr Asn Lys Pro Val Leu Gly Ala		
145	150	155
Ala Leu Thr Val Ile Ser Gly Arg Ser Ser Pro Met Asp Val Val Arg		
165	170	175
Val Gln Leu Gln Ser Arg Ser Leu Tyr Ser Phe Leu Ser Ile Gly Trp		
180	185	190
Gly Leu Ile Ser Asp Val Asp Ile Glu Ser Glu Arg Ile Arg Met Leu		
195	200	205
Gly Tyr Gln Arg Phe Thr Val Trp Thr Leu Tyr Arg Leu Val Asn Leu		
210	215	220
Arg Thr Tyr Asn Gly Arg Ile Ser Tyr Leu Leu Thr Asp His Glu Val		
225	230	235
Ser Ser Thr His Ser Ala Thr Gly Tyr Ala Ala Gln Arg Arg Met Gln		
245	250	255
Ser Ser Arg Ser Cys Asn Thr His Ile Asp Met Leu Asn Gly Pro Ala		
260	265	270
Pro Ile Tyr His Ser Ser Ala Glu Tyr Leu Pro Gln Glu Phe Ala Asp		
275	280	285
Val Ile Ser Leu Glu Thr Ser Ile Asn Gln Ser Phe Arg Ser Arg Cys		

290	295	300
Asp Ser Trp Leu Ser Gly	Gly Ser Arg Arg Ser	Phe Tyr Tyr Ser Ile
305	310	315
Ser Glu Ser Ile Tyr His Ser Leu Ala Asp	Glu Ser Glu Phe Ala Gly	320
325	330	335
Leu Ala Ala Ala Ser Leu Glu Asn Arg Gln	Gln Asn Tyr Gly Pro Ala	
340	345	350
Ser Glu Leu Pro Asp Leu Asn Glu Pro	Leu Ser Glu Asp Gln Gly Trp	
355	360	365
Leu Val Glu Glu Gly Glu	Phe Val Met Met His Ala Val Tyr Gln Thr	
370	375	380
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385	390	395
Gly Thr Ile Tyr Leu Ile Leu Ile Arg Ala	Gly Ile Ser Arg Pro His	
405	410	415
Leu Leu Ser Phe Leu Tyr Asn Met Ser	Ser Gly Thr His Leu Pro Glu	
420	425	430
Ser His Asp Asp His Val Lys Val	Leu Pro Val Arg Ala Phe Arg Leu	
435	440	445
Glu Pro Tyr Asp Asn His Gly Ile Ile	Thr Val Asp Gly Glu Arg Val	
450	455	460
Glu Phe Gly Pro Leu Gln Ala Glu Val	Leu Pro Gly Ile Ala Arg Val	
465	470	475
Met Val Pro Asn Val Ser Thr Phe Arg	Phe Gln Ser Ala Thr Leu Gln	
485	490	495
His Gly Ile Pro Val Cys Ile Pro Val Arg	Lys Arg Phe Val Leu Tyr	
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Asn Met Ser Ser Glu Glu Leu Ala Pro	Ile Asn Glu	
515	520	

<210> 21
<211> 368
<212> PRT
<213> Homo sapiens

<400> 21

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20	25	30	
Phe Thr Leu Met Leu Thr Glu Arg	Arg Asn His Ala Arg Glu Leu Val		
35	40	45	
Arg Ser Glu Glu Leu Gly Arg Trp Asp	Ala Leu Val Val Met Ser Gly		
50	55	60	
Asp Gly Leu Met His Glu Val Val Asn	Gly Leu Met Glu Arg Pro Asp		
65	70	75	80
Trp Glu Thr Ala Ile Gln Lys Pro	Leu Cys Ser Leu Pro Ala Gly Ser		
85	90	95	
Gly Asn Ala Leu Ala Ala Ser Leu Asn	His Tyr Ala Gly Tyr Glu Gln		
100	105	.	110
Val Thr Asn Glu Asp Leu Leu Thr Asn	Cys Thr Leu Leu Leu Cys Arg		
115	120	125	
Arg Leu Leu Ser Pro Met Asn Leu	Leu Ser Leu His Thr Ala Ser Gly		

130	135	140
Leu Arg Leu Phe Ser Val	Leu Ser Leu Ala Trp	Gly Phe Ile Ala Asp
145	150	155
Val Asp Leu Glu Ser	Glu Lys Tyr Arg Arg	Leu Gly Glu Met Arg Phe
	165	170
Thr Leu Gly Thr Phe Leu Arg	Leu Ala Ala Leu Arg	Thr Tyr Arg Gly
	180	185
Arg Leu Ala Tyr Leu Pro Val	Gly Arg Val Gly Ser	Lys Thr Pro Ala
	195	200
Ser Pro Val Val Val Gln	Gln Gly Pro Val Asp	Ala His Leu Val Pro
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Leu Glu Glu Pro Val Pro	Ser His Trp Thr Val Val	Pro Asp Glu Asp
	225	230
Phe Val Leu Val Leu Ala	Leu His Ser His Leu Gly	Ser Glu Met
	245	250
Phe Ala Ala Pro Met Gly Arg Cys	Ala Ala Gly Val Met	His Leu Phe
	260	265
Tyr Val Arg Ala Gly Val Ser	Arg Ala Met Leu Leu Arg	Leu Phe Leu
	275	280
Ala Met Glu Lys Gly Arg His	Met Glu Tyr Glu Cys	Pro Tyr Leu Val
	290	295
Tyr Val Pro Val Val Ala Phe Arg	Leu Glu Pro Lys Asp	Gly Lys Gly
	305	310
Val Phe Ala Val Asp Gly	Glu Leu Met Val Ser	Glu Ala Val Gln Gly
	325	330
Gln Val His Pro Asn Tyr Phe Trp	Met Val Ser Gly Cys	Val Glu Pro
	340	345
Pro Pro Ser Trp Lys Pro Gln	Gln Met Pro Pro Pro	Glu Glu Pro Leu
	355	360
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<210> 22
<211> 1152
<212> DNA
<213> Homo sapiens

<400> 22

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 <213> Homo sapiens

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 <211> 2629
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 <213> Drosophila melanogaster

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<212> DNA
<213> Dros

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 Val Tyr Leu Arg Arg Glu Thr Glu Glu Asp Asp His Ile Asn Glu Gln
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 Lys Lys Arg Ala Arg Gly Gly Leu Asn Ser Cys Arg Asn Pro Asn Val
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 Pro Gly Gln Glu Ala Asp Ser Glu Pro Asp Ser Asp Asn Ser Ala Tyr
 115 120 125
 Leu Tyr Ile Tyr Ala Tyr Leu Lys Lys Glu Lys Pro Leu Arg Arg Val
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 Asn Leu Gln Thr Ala Glu Met Trp His His Thr Ile Arg Lys His Lys
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 Ile Leu Leu Asn Pro Lys Ser Gly Ser Gly Lys Gly Arg Glu Leu Phe
 195 200 205
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 210 215 220
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 245 250 255
 Asp Gly Leu Phe Tyr Glu Val Leu Asn Gly Leu Met Glu Arg Met Asp
 260 265 270
 Trp Arg Arg Ala Cys Arg Glu Leu Pro Leu Gly Ile Ile Pro Cys Gly
 275 280 285
 Ser Gly Asn Gly Leu Ala Lys Ser Val Ala His His Cys Asn Glu Pro
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Tyr Glu Pro Lys Pro Ile Leu His Ala Thr Leu Thr Cys Met Ala Gly
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 Lys Ser Thr Pro Met Asp Val Val Arg Val Glu Leu Ala Thr Arg Asp
 325 330 335
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 370 375 380
 Lys Gly Arg Val Ser Tyr Leu Leu Gly Lys Gly Lys Lys Glu Pro Pro
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 Glu Glu Glu Gly Glu Ala Val Leu Asp Gly Glu Gln Phe Ala Asp Ala
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 485 490 495
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 565 570 575
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 595 600 605
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<212> PRT

<213> Drosophila melanogaster

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 65 70 75 80
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 85 90 95
 Gly Ala Cys Ala Cys Ser Ser Gly Asn Pro Asn Ser Pro Ala Ile Ser
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 Ala Ser Gly Asp His His Arg Pro Ala Thr Thr Pro Ser Lys Cys Ser
 115 120 125
 Thr Asn Ser Arg Asp Asn Ile Pro Ser Asp Gly Gly Asp Val Ser Ala
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 Phe Leu Tyr Val Phe Ala Tyr Val Leu Lys Lys Arg Ser Leu Arg Ser
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 Asp Thr Phe Glu Asp Asn Met Arg Glu Ala Asp Arg Trp Tyr Arg Ser
 180 185 190
 Leu Arg Trp Gln Leu His Arg Thr Leu Glu Glu Ile Phe Val Ala Pro
 195 200 205
 Thr Val Asp Glu Arg Arg Arg Val Leu Val Leu Leu Asn Pro Lys
 210 215 220
 Ser Gly Ser Gly Asp Ala Arg Glu Val Phe Asn Met His Val Thr Pro
 225 230 235 240
 Val Leu Asn Glu Ala Glu Val Pro Tyr Asp Leu Tyr Val Thr Lys His
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 Cys Cys Val Val Ala Val Gly Gly Asp Gly Leu Phe His Glu Ile Val
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 Ala Lys Asn His Ser Ser Glu Arg Asp Ile Asp Glu Leu Thr Arg Phe
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 835 840 845
 His Phe Pro Glu Arg Leu Gly Val Cys Leu Ile Ile Asn Ser Pro Gly
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 Leu Phe Ser Thr Ile Trp Pro Ala Ile Arg Val Leu Leu Asp Asp Asn
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 Ile Ser Ser Asn Pro Phe Gln Thr Glu Asn Leu Ser Ser Ser Glu
 100 105 110
 Asn Asp Asp Val Glu Asn His Ser Leu Ser Asn Asp Lys Ala Pro Val
 115 120 125
 Ser Glu Ser Gln Ser Phe Pro Lys Lys Asp Lys Trp Asp Thr Lys Thr
 130 135 140
 Asn Thr Val Lys Val Ser Pro Asp Asp Ser Gln Asp Asn Ser Pro Ser
 145 150 155 160
 Leu Gly Ile Lys Asp Asn Gln Gln Leu Ile Glu Leu Thr Phe Ala Val
 165 170 175
 Pro Lys Gly His Asp Val Ile Pro Gln Lys Leu Thr Leu Leu Ile Asp
 180 185 190
 His Val Ser Arg Lys Ser Arg Ala Asn Thr Gly Glu Glu Asn Ile Ser
 195 200 205
 Ser Gly Thr Val Glu Glu Ile Leu Glu Lys Ser Tyr Glu Asn Ser Lys
 210 215 220
 Arg Asn Arg Ser Ile Leu Val Ile Ile Asn Pro His Gly Gly Lys Gly
 225 230 235 240
 Thr Ala Lys Asn Leu Phe Leu Thr Lys Ala Arg Pro Ile Leu Val Glu
 245 250 255
 Ser Gly Cys Lys Ile Glu Ile Ala Tyr Thr Lys Tyr Ala Arg His Ala
 260 265 270
 Ile Asp Ile Ala Lys Asp Leu Asp Ile Ser Lys Tyr Asp Thr Ile Ala
 275 280 285
 Cys Ala Ser Gly Asp Gly Ile Pro Tyr Glu Val Ile Asn Gly Leu Tyr
 290 295 300
 Arg Arg Pro Asp Arg Val Asp Ala Phe Asn Lys Leu Ala Val Thr Gln
 305 310 315 320
 Leu Pro Cys Gly Ser Gly Asn Ala Met Ser Ile Ser Cys His Trp Thr
 325 330 335
 Asn Asn Pro Ser Tyr Ala Ala Leu Cys Leu Val Lys Ser Ile Glu Thr
 340 345 350
 Arg Ile Asp Leu Met Cys Cys Ser Gln Pro Ser Tyr Met Asn Glu Trp
 355 360 365
 Pro Arg Leu Ser Phe Leu Ser Gln Thr Tyr Gly Val Ile Ala Glu Ser
 370 375 380
 Asp Ile Asn Thr Glu Phe Ile Arg Trp Met Gly Pro Val Arg Phe Asn
 385 390 395 400
 Leu Gly Val Ala Phe Asn Ile Ile Gln Gly Lys Lys Tyr Pro Cys Glu
 405 410 415
 Val Phe Val Lys Tyr Ala Ala Lys Ser Lys Lys Glu Leu Lys Val His
 420 425 430
 Phe Leu Glu Asn Lys Asp Lys Asn Lys Gly Cys Leu Thr Phe Glu Pro
 435 440 445

Asn	Pro	Ser	Pro	Asn	Ser	Ser	Pro	Asp	Leu	Leu	Ser	Lys	Asn	Asn	Ile
						450									
							455								
Asn	Asn	Ser	Thr	Lys	Asp	Glu	Leu	Ser	Pro	Asn	Phe	Leu	Asn	Glu	Asp
						465									
							470								
											475				
Asn	Phe	Lys	Leu	Lys	Tyr	Pro	Met	Thr	Glu	Pro	Val	Pro	Arg	Asp	Trp
							485								
									490						
Glu	Lys	Met	Asp	Ser	Glu	Leu	Thr	Asp	Asn	Leu	Thr	Ile	Phe	Tyr	Thr
							500								
								505							
Gly	Lys	Met	Pro	Tyr	Ile	Ala	Lys	Asp	Thr	Lys	Phe	Phe	Pro	Ala	Ala
							515								
								520							
Leu	Pro	Ala	Asp	Gly	Thr	Ile	Asp	Leu	Val	Ile	Thr	Asp	Ala	Arg	Ile
							530								
								535							
Pro	Val	Thr	Arg	Met	Thr	Pro	Ile	Leu	Leu	Ser	Leu	Asp	Lys	Gly	Ser
							545								
								550							
His	Val	Leu	Glu	Pro	Glu	Val	Ile	His	Ser	Lys	Ile	Leu	Ala	Tyr	Lys
								565							
									570						
Ile	Ile	Pro	Lys	Val	Glu	Ser	Gly	Leu	Phe	Ser	Val	Asp	Gly	Glu	Lys
								580							
									585						
Phe	Pro	Leu	Glu	Pro	Leu	Gln	Val	Glu	Ile	Met	Pro	Met	Leu	Cys	Lys
								595							
									600						
Thr	Leu	Leu	Arg	Asn	Gly	Arg	Tyr	Ile	Asp	Thr	Glu	Phe	Glu	Ser	Met
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									615						
											620				

<210> 32
<211> 2064
<212> DNA
<213> Sacc

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gatgacgaag actcccaactt gatatctcgat gatctggcag attctagtgc tgatcaaatt 1620
aaagaggaag atttcaaaat aaaatatcca ttagatgaag gtatccctag tgactggaa 1680
agattggatc ctaatatttc gaacaaccta ggtatcttct atacggtaa aatgccatat 1740
gtggctgctg acactaaatt ctccggca gcgcttcctt cagatggcac aatccctgcg 1800
gttataccg atgcaagaac ctcgttgacg aggatggcac caatccctgcg 1860
aagggttccc atgtttaca accggaagtc ttacactcta aaattttggc atacaagata 1920
ataccaaagc tagggAACGG ctgttctct gtcgatggcg agaaatttcc tctagagccc 1980
cttcaagtcg aaattatgcc acgcttatgc aagacgttac tgagaaatgg ccgttatgtg 2040
gacacagatt tcgattctat gtga 2064

<210> 33

<211> 687

<212> PRT

<213> Saccharomyces cerevisiae

<400> 33

Met	Thr	Leu	Lys	Pro	Ser	Lys	Arg	Arg	Lys	Gly	Arg	Ser	Arg	His	Ser
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Arg	Lys	Lys	Gln	Ile	Thr	Ser	Ala	Ile	Leu	Thr	Glu	Glu	Gly	Ile	Met
									20		25			30	
Ile	Lys	Ala	Lys	Pro	Ser	Ser	Pro	Tyr	Thr	Tyr	Ala	Asn	Arg	Met	Ala
									35		40			45	
Asp	Lys	Arg	Ser	Arg	Ser	Ser	Ile	Asp	Asn	Ile	Ser	Arg	Thr	Ser	Phe
								50		55			60		
Gln	Ser	Asn	Ile	Ser	Arg	Thr	Ser	Phe	Gln	Ser	Asn	Ser	Asp	Asn	Asn
								65		70			75		80
Ser	Ile	Phe	Glu	Thr	Ala	Ser	Leu	Ile	Ser	Cys	Val	Thr	Cys	Leu	Ser
								85		90			95		
Asp	Thr	Asp	Thr	Ile	Asp	Arg	Ser	Glu	Thr	Ser	Thr	Thr	Asp	Thr	Ser
								100		105			110		
Lys	Asp	Asp	Leu	Ser	Ala	Asn	Pro	Lys	Leu	His	Tyr	Pro	Ser	Val	Asn
								115		120			125		
Gly	Gln	Leu	Pro	Ala	Asn	Thr	Val	Ile	Pro	Tyr	Gly	Arg	Ile	Leu	Asp
								130		135			140		
Ala	Arg	Tyr	Ile	Glu	Lys	Glu	Pro	Leu	His	Tyr	Tyr	Asp	Ala	Asn	Ser
								145		150			155		160
Ser	Pro	Ser	Pro	Leu	Ser	Ser	Ser	Met	Ser	Asn	Ile	Ser	Glu	Lys	
								165		170			175		
Cys	Asp	Leu	Asp	Glu	Leu	Glu	Ser	Ser	Gln	Lys	Lys	Glu	Arg	Lys	Gly
								180		185			190		
Asn	Ser	Leu	Ser	Arg	Gly	Ser	Asn	Ser	Ser	Ser	Ser	Leu	Leu	Thr	Ser
								195		200			205		
Arg	Ser	Pro	Phe	Thr	Lys	Leu	Val	Glu	Val	Ile	Phe	Ala	Arg	Pro	Arg
								210		215			220		
Arg	His	Asp	Val	Val	Pro	Lys	Arg	Val	Ser	Leu	Tyr	Ile	Asp	Tyr	Lys
								225		230			235		240
Pro	His	Ser	Ser	His	Leu	Lys	Glu	Glu	Asp	Asp	Leu	Val	Glu	Glu	
								245		250			255		
Ile	Leu	Lys	Arg	Ser	Tyr	Lys	Asn	Thr	Arg	Arg	Asn	Lys	Ser	Ile	Phe
								260		265			270		
Val	Ile	Ile	Asn	Pro	Phe	Gly	Gly	Lys	Gly	Lys	Ala	Lys	Lys	Leu	Phe
								275		280			285		

Met Thr Lys Ala Lys Pro Leu Leu Leu Ala Ser Arg Cys Ser Ile Glu
 290 295 300
 Val Val Tyr Thr Lys Tyr Pro Gly His Ala Ile Glu Ile Ala Arg Glu
 305 310 315 320
 Met Asp Ile Asp Lys Tyr Asp Thr Ile Ala Cys Ala Ser Gly Asp Gly
 325 330 335
 Ile Pro His Glu Val Ile Asn Gly Leu Tyr Gln Arg Pro Asp His Val
 340 345 350
 Lys Ala Phe Asn Asn Ile Ala Ile Thr Glu Ile Pro Cys Gly Ser Gly
 355 360 365
 Asn Ala Met Ser Val Ser Cys His Trp Thr Asn Asn Pro Ser Tyr Ser
 370 375 380
 Thr Leu Cys Leu Ile Lys Ser Ile Glu Thr Arg Ile Asp Leu Met Cys
 385 390 395 400
 Cys Ser Gln Pro Ser Tyr Ala Arg Glu His Pro Lys Leu Ser Phe Leu
 405 410 415
 Ser Gln Thr Tyr Gly Leu Ile Ala Glu Thr Asp Ile Asn Thr Glu Phe
 420 425 430
 Ile Arg Trp Met Gly Pro Ala Arg Phe Glu Leu Gly Val Ala Phe Asn
 435 440 445
 Ile Ile Gln Lys Lys Tyr Pro Cys Glu Ile Tyr Val Lys Tyr Ala
 450 455 460
 Ala Lys Ser Lys Asn Glu Leu Lys Asn His Tyr Leu Glu His Lys Asn
 465 470 475 480
 Lys Gly Ser Leu Glu Phe Gln His Ile Thr Met Asn Lys Asp Asn Glu
 485 490 495
 Asp Cys Asp Asn Tyr Asn Tyr Glu Asn Glu Tyr Glu Thr Glu Asn Glu
 500 505 510
 Asp Glu Asp Glu Asp Ala Asp Asp Asp Glu Asp Ser His Leu Ile
 515 520 525
 Ser Arg Asp Leu Ala Asp Ser Ser Ala Asp Gln Ile Lys Glu Glu Asp
 530 535 540
 Phe Lys Ile Lys Tyr Pro Leu Asp Glu Gly Ile Pro Ser Asp Trp Glu
 545 550 555 560
 Arg Leu Asp Pro Asn Ile Ser Asn Asn Leu Gly Ile Phe Tyr Thr Gly
 565 570 575
 Lys Met Pro Tyr Val Ala Ala Asp Thr Lys Phe Phe Pro Ala Ala Leu
 580 585 590
 Pro Ser Asp Gly Thr Met Asp Met Val Ile Thr Asp Ala Arg Thr Ser
 595 600 605
 Leu Thr Arg Met Ala Pro Ile Leu Leu Gly Leu Asp Lys Gly Ser His
 610 615 620
 Val Leu Gln Pro Glu Val Leu His Ser Lys Ile Leu Ala Tyr Lys Ile
 625 630 635 640
 Ile Pro Lys Leu Gly Asn Gly Leu Phe Ser Val Asp Gly Glu Lys Phe
 645 650 655
 Pro Leu Glu Pro Leu Gln Val Glu Ile Met Pro Arg Leu Cys Lys Thr
 660 665 670
 Leu Leu Arg Asn Gly Arg Tyr Val Asp Thr Asp Phe Asp Ser Met
 675 680 685

<212> DNA

<213> Saccharomyces cerevisiae

<400> 34

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 cgaactcgaa tgtccaaatt tcggtttaat attagagaga agctgttagt gtttaccaac 180
 aatcaatcat tcacattaag ccgctggcaa aagaagtacc gttctgcgtt taatgatctc 240
 tacttactt atacttcctt aatgggatcg catacctct atgttctgtg tttacctatg 300
 cccgtgtgg tttggatattt tgaaacaaca aaagatatgg tttatatctt gggatattct 360
 atctacttga gtggttttt taaagattac tggtgcttc ccaggcctag agcaccccca 420
 ttacatcgaa ttacgttaag tgaatataca acgaaggaat atgggtctcc aagctccat 480
 acagcaaatg caacaggagt gagtctctt tttctctaca acatctggag gatgcaagaa 540
 tcttctgtca tggtccaact atggtgtca tgggtgttt tattttatta tatgacttt 600
 gtttccgta gaatatactg tggatgcat ggcattttttt attagtaag cggtgggctc 660
 attggaatag tgtgtttcat tggtagatg tatttcaagt acaggttcc gggttacgc 720
 attgaggagc attgggggtt tcctttgtt agtggggat ggggtcttc tctttgttt 780
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 gttgtgtcag gtattgaatg ctgtgattgg ttggcaag tgtttgaggt caccctggg 900
 tacaatttgg aacctaactg tggctggcg ttaaccttag ccaggctgct ggtggcccta 960
 ccgtgcgtt ttatctggaa gtacgtgatc agcaaaccga tgatctacac gttattgatc 1020
 aaagtttcc atctgaagga tgacagaaac gttcggcaa gaaaaagact ggaggccacg 1080
 cacaagaag gtcaagcaa gtacgaatgt ccattatata ttggagagcc caagattgac 1140
 attctaggta gatttattat ctatgctggc gttccattca ccgttgaat gtgcagcccc 1200
 gtcctatccc ccctctaaa tatagcataa 1230

<210> 35

<211> 409

<212> PRT

<213> Saccharomyces cerevisiae

<400> 35

Met	Val	Asp	Gly	Leu	Asn	Thr	Ser	Asn	Ile	Arg	Lys	Arg	Ala	Arg	Thr
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Leu	Ser	Asn	Pro	Asn	Asp	Phe	Gln	Glu	Pro	Asn	Tyr	Leu	Leu	Asp	Pro
								20			25			30	
Gly	Asn	His	Pro	Ser	Asp	His	Phe	Arg	Thr	Arg	Met	Ser	Lys	Phe	Arg
								35			40		45		
Phe	Asn	Ile	Arg	Glu	Lys	Leu	Leu	Val	Phe	Thr	Asn	Asn	Gln	Ser	Phe
								50			55		60		
Thr	Leu	Ser	Arg	Trp	Gln	Lys	Lys	Tyr	Arg	Ser	Ala	Phe	Asn	Asp	Leu
								65			70		75		80
Tyr	Phe	Thr	Tyr	Thr	Ser	Leu	Met	Gly	Ser	His	Thr	Phe	Tyr	Val	Leu
								85			90		95		
Cys	Leu	Pro	Met	Pro	Val	Trp	Phe	Gly	Tyr	Phe	Glu	Thr	Thr	Lys	Asp
								100			105		110		
Met	Val	Tyr	Ile	Leu	Gly	Tyr	Ser	Ile	Tyr	Leu	Ser	Gly	Phe	Phe	Lys
								115			120		125		
Asp	Tyr	Trp	Cys	Leu	Pro	Arg	Pro	Arg	Ala	Pro	Pro	Leu	His	Arg	Ile
								130			135		140		
Thr	Leu	Ser	Glu	Tyr	Thr	Thr	Lys	Glu	Tyr	Gly	Ala	Pro	Ser	Ser	His
								145			150		155		160
Thr	Ala	Asn	Ala	Thr	Gly	Val	Ser	Leu	Leu	Phe	Leu	Tyr	Asn	Ile	Trp
								165			170		175		

Arg Met Gln Glu Ser Ser Val Met Val Gln Leu Leu Leu Ser Cys Val
 180 185 190
 Val Leu Phe Tyr Tyr Met Thr Leu Val Phe Gly Arg Ile Tyr Cys Gly
 195 200 205
 Met His Gly Ile Leu Asp Leu Val Ser Gly Gly Leu Ile Gly Ile Val
 210 215 220
 Cys Phe Ile Val Arg Met Tyr Phe Lys Tyr Arg Phe Pro Gly Leu Arg
 225 230 235 240
 Ile Glu Glu His Trp Trp Phe Pro Leu Phe Ser Val Gly Trp Gly Leu
 245 250 255
 Leu Leu Leu Phe Lys His Val Lys Pro Val Asp Glu Cys Pro Cys Phe
 260 265 270
 Gln Asp Ser Val Ala Phe Met Gly Val Val Ser Gly Ile Glu Cys Cys
 275 280 285
 Asp Trp Leu Gly Lys Val Phe Gly Val Thr Leu Val Tyr Asn Leu Glu
 290 295 300
 Pro Asn Cys Gly Trp Arg Leu Thr Leu Ala Arg Leu Leu Val Gly Leu
 305 310 315 320
 Pro Cys Val Val Ile Trp Lys Tyr Val Ile Ser Lys Pro Met Ile Tyr
 325 330 335
 Thr Leu Leu Ile Lys Val Phe His Leu Lys Asp Asp Arg Asn Val Ala
 340 345 350
 Ala Arg Lys Arg Leu Glu Ala Thr His Lys Glu Gly Ala Ser Lys Tyr
 355 360 365
 Glu Cys Pro Leu Tyr Ile Gly Glu Pro Lys Ile Asp Ile Leu Gly Arg
 370 375 380
 Phe Ile Ile Tyr Ala Gly Val Pro Phe Thr Val Val Met Cys Ser Pro
 385 390 395 400
 Val Leu Phe Ser Leu Leu Asn Ile Ala
 405

<210> 36
 <211> 1215
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 36
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 atggctcctt ccggcgccaa acacctattt gcagatcccg gtaatcatcc agcggagcat 120
 tttgagagcc agatgtcg t gctaaggttt caaacaaggc agtatctaac tagattcaca 180
 gacaaccaat cagatttcgt acattctta caaaaaaaggc acagaacgc tttagagac 240
 gtttatttca aatacacttc gcttatgggt tcccacatgt tttatgttat cgtgcttccc 300
 atgcctgtgt ggcttgata ccgcgattt aacacggaca tgatctacgt tcttggttat 360
 tcaatttatt tgagtggcta cttaaaggat tattgggcc tccaaggcc aaaatcaccg 420
 ccagttgaca gaatcacact aagtgaatac actacgaaag aatatggtgc acccagttca 480
 cattctgcta acgctactgc ggttaagtcta ttattttt ggagaatatg tttatctgac 540
 acactggat ggcacaaa gcttctttt ctgagttcg tgatatttta ctacttaacc 600
 ctggttttt gtagagttt ctgcggatgc catggatgc tggattttt tagcggcgcc 660
 gcagttggag ctatctgtt ttttataaga atctgggtgg tgcattgc ttttac 720
 cagattggtg aacatctctg gtcccccctt ttgagttcg catgggtttt gtttattctg 780
 tttaaccacg tcaggccat ttagtgaatgt ccttgcgttgc aagatagcgt agcgttcatt 840
 ggcgttagtca gtgggctgga ttgcagcgcac tggtaaccg aaagatacgg atgaaacctt 900
 gtagttagta ggtacgcattc atgtggttct aaggtgttct tgaggcctct ggttagtgc 960

gcttctgtga ttgtttggaa agacgtcatt agcaagacag ctgtctcacac gctgttaatt 1020
 aaactactca gattcacga ttagatagaagc gaaaagggttc atttccataa cgagacaagt 1080
 gaagaagaag agtgttatt gtacagcggt gtttccaaag tggaaatcggt cggaagggtt 1140
 ctcatacgt caggtatacc tacaaccgtc ttttgctat gcccagttt tttcacttgg 1200
 acaaacttaa ggtag 1215

<210> 37
 <211> 404
 <212> PRT
 <213> *Sacchromyces cerevisiae*

<400> 37
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 Ile Lys Val Gln Met Ala Pro Ser Gly Gly Lys His Leu Leu Ala Asp
 20 25 30
 Pro Gly Asn His Pro Ala Glu His Phe Glu Ser Gln Met Ser Trp Leu
 35 40 45
 Arg Phe Gln Thr Arg Gln Tyr Leu Thr Arg Phe Thr Asp Asn Gln Ser
 50 55 60
 Asp Phe Val His Ser Leu Gln Lys Lys His Arg Thr Pro Phe Arg Asp
 65 70 75 80
 Val Tyr Phe Lys Tyr Thr Ser Leu Met Gly Ser His Met Phe Tyr Val
 85 90 95
 Ile Val Leu Pro Met Pro Val Trp Leu Gly Tyr Arg Asp Leu Thr Arg
 100 105 110
 Asp Met Ile Tyr Val Leu Gly Tyr Ser Ile Tyr Leu Ser Gly Tyr Leu
 115 120 125
 Lys Asp Tyr Trp Cys Leu Pro Arg Pro Lys Ser Pro Pro Val Asp Arg
 130 135 140
 Ile Thr Leu Ser Glu Tyr Thr Lys Glu Tyr Gly Ala Pro Ser Ser
 145 150 155 160
 His Ser Ala Asn Ala Thr Ala Val Ser Leu Leu Phe Phe Trp Arg Ile
 165 170 175
 Cys Leu Ser Asp Thr Leu Val Trp Pro Thr Lys Leu Leu Leu Leu Ser
 180 185 190
 Leu Val Ile Phe Tyr Tyr Leu Thr Leu Val Phe Gly Arg Val Tyr Cys
 195 200 205
 Gly Met His Gly Met Leu Asp Leu Phe Ser Gly Ala Ala Val Gly Ala
 210 215 220
 Ile Cys Phe Phe Ile Arg Ile Trp Val Val His Ala Leu Arg Asn Phe
 225 230 235 240
 Gln Ile Gly Glu His Leu Trp Phe Pro Leu Leu Ser Val Ala Trp Gly
 245 250 255
 Leu Phe Ile Leu Phe Asn His Val Arg Pro Ile Asp Glu Cys Pro Cys
 260 265 270
 Phe Glu Asp Ser Val Ala Phe Ile Gly Val Val Ser Gly Leu Asp Cys
 275 280 285
 Ser Asp Trp Leu Thr Glu Arg Tyr Gly Trp Asn Leu Val Cys Ser Arg
 290 295 300
 Tyr Ala Ser Cys Gly Ser Lys Val Phe Leu Arg Pro Leu Val Gly Val
 305 310 315 320
 Ala Ser Val Ile Val Trp Lys Asp Val Ile Ser Lys Thr Ala Val Tyr
 325 330 335

Thr Leu Leu Ile Lys Leu Leu Arg Phe His Asp Asp Arg Ser Glu Lys
 340 345 350
 Val His Phe His Asn Glu Thr Ser Glu Glu Glu Cys Leu Leu Tyr
 355 360 365
 Ser Gly Val Ser Lys Val Glu Ile Val Gly Arg Phe Leu Ile Tyr Ala
 370 375 380
 Gly Ile Pro Thr Thr Val Phe Leu Leu Cys Pro Val Phe Phe Thr Trp
 385 390 395 400
 Thr Asn Leu Arg

<210> 38
 <211> 1050
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 38
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 tccttgctgc cgaaatgtag tgatgggtgt ctggccttgg ttgcgcgggt tggtgcctac 180
 tggcggtgt ctggtatatt ccatgtaata gacacttcc atctggctga gaagtacaga 240
 attcatccga gcgaagaggt tgccaagagg aacaaggcgt cgagaatgca tgtttcctt 300
 gaagtgatttacaacatatacatacagacc attgttgcc ttatctttat gcacttcgag 360
 ccgatctaca tgactgggtt tgaagaaaaat gccatgttgc agcttcgtgc agacccctt 420
 cgatttatttccatgcccgc tattttattac ggctatatgt acggaatgtc cgcttgaag 480
 atctttgcag gcttttattt cgttgataca tggcaatact ttttgcatac attgtatgc 540
 atgaataaga ctttatacaa atggttccac tctgttcatc atgaactata cgtgcctat 600
 gcttacggtg ctctttcaa caatcctgtt gagggcttct tgtagatac ttgggaacc 660
 ggtattgcca tgacgttaac tcatttgact cacagagagc aaatcattct ttttacctt 720
 gccaccatga agactgtcga tgaccactgt ggtatgctt tgccacttgc cccatccaa 780
 tggctttcc ctaataacgc tggctatcac gatatccacc accagcaatt tggtatcaag 840
 acgaacttttgc tcaaccatt ttcaactttc tggacaatt tggtccaaac taacttaaa 900
 ggtttgaag aatataaaaa gaagcaaaaga cgtgtcacca tcgacaagta caaagagttt 960
 ttgcaagaga gagaatttggaa aaagaaggag aaactaaaa acttcaaaagc tatgaatgct 1020
 gctgaaaatg aagtaaagaa agagaaataa 1050

<210> 39
 <211> 349
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 39
 Met Asn Val Thr Ser Asn Ala Thr Ala Ala Gly Ser Phe Pro Leu Ala
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 Phe Gly Leu Lys Thr Ser Phe Gly Phe Met His Tyr Ala Lys Ala Pro
 20 25 30
 Ala Ile Asn Leu Arg Pro Lys Glu Ser Leu Leu Pro Glu Met Ser Asp
 35 40 45
 Gly Val Leu Ala Leu Val Ala Pro Val Val Ala Tyr Trp Ala Leu Ser
 50 55 60
 Gly Ile Phe His Val Ile Asp Thr Phe His Leu Ala Glu Lys Tyr Arg
 65 70 75 80
 Ile His Pro Ser Glu Glu Val Ala Lys Arg Asn Lys Ala Ser Arg Met

85	90	95
His Val Phe Leu Glu Val Ile Leu Gln His Ile Ile Gln Thr Ile Val		
100	105	110
Gly Leu Ile Phe Met His Phe Glu Pro Ile Tyr Met Thr Gly Phe Glu		
115	120	125
Glu Asn Ala Met Trp Lys Leu Arg Ala Asp Leu Pro Arg Ile Ile Pro		
130	135	140
Asp Ala Ala Ile Tyr Tyr Gly Tyr Met Tyr Gly Met Ser Ala Leu Lys		
145	150	155
Ile Phe Ala Gly Phe Leu Phe Val Asp Thr Trp Gln Tyr Phe Leu His		
165	170	175
Arg Leu Met His Met Asn Lys Thr Leu Tyr Lys Trp Phe His Ser Val		
180	185	190
His His Glu Leu Tyr Val Pro Tyr Ala Tyr Gly Ala Leu Phe Asn Asn		
195	200	205
Pro Val Glu Gly Phe Leu Leu Asp Thr Leu Gly Thr Gly Ile Ala Met		
210	215	220
Thr Leu Thr His Leu Thr His Arg Glu Gln Ile Ile Leu Phe Thr Phe		
225	230	235
Ala Thr Met Lys Thr Val Asp Asp His Cys Gly Tyr Ala Leu Pro Leu		
245	250	255
Asp Pro Phe Gln Trp Leu Phe Pro Asn Asn Ala Val Tyr His Asp Ile		
260	265	270
His His Gln Gln Phe Gly Ile Lys Thr Asn Phe Ala Gln Pro Phe Phe		
275	280	285
Thr Phe Trp Asp Asn Leu Phe Gln Thr Asn Phe Lys Gly Phe Glu Glu		
290	295	300
Tyr Gln Lys Lys Gln Arg Arg Val Thr Ile Asp Lys Tyr Lys Glu Phe		
305	310	315
Leu Gln Glu Arg Glu Leu Glu Lys Lys Glu Lys Leu Lys Asn Phe Lys		
325	330	335
Ala Met Asn Ala Ala Glu Asn Glu Val Lys Lys Glu Lys		
340	345	

<210> 40
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 40
atattaagct tatggatcca gcgggcggcc cc

32

<210> 41
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 41
agatctagat cataaggcgt cttctggcgg 30